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(54) Title: ADAMTS13 GENES AND PROTEINS AND VARIANTS, AND USES THEREOF

(57) Abstract: The present invention relates to a disintegrin and metalloproteinase containing thrombospondin 1-like domains (ADAMTS) and in particular to a novel ADAMTS13 protease and to nucleic acids encoding ADAMTS13 proteases. The present invention encompasses both native and recombinant wild-type forms of ADAMTS13, as well as mutant and variant forms including fragments, some of which posses altered characteristics relative to the wild-type ADAMTS13. The present invention also relates to methods of using ADAMTS13, including for treatment of TTP. The present invention also relates to methods for screening for the presence of TTP. The present invention further relates to methods for developing antiocoagulant drugs based upon ADAMTS13.

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ADAMTS13 GENES AND PROTEINS AND VARIANTS, AND USES THEREOF

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The present application claims priority from provisional application Serial No. 60/312,834, filed August 16, 2001.

FIELD OF THE INVENTION

The present invention relates to a disintegrin and metalloproteinase containing thrombospondin 1-like domains (ADAMTS), and in particular to a novel ADAMTS13 protease and to nucleic acids encoding ADAMTS13 proteases, and to methods of using the same.

BACKGROUND OF THE INVENTION

Thrombotic Thrombocytopenic Purpura (TTP) is a disorder of the blood characterized by low platelets, low red blood cell count (caused by premature breakdown of the cells), and neurological abnormalities. The sharp drop in the number of red blood cells and platelets in the blood is associated with severe problems affecting the kidneys and brain, along with fever and bleeding. Purpura refers to the characteristic bleeding that occurs beneath the skin, or in mucus membranes, which produces bruises, or a red rash-like appearance; the bleeding can be catastrophic. The neurological symptoms associated with this disease include headaches, confusion, speech changes, and alterations in consciousness, which vary from lethargy to coma; other symptoms include development of kidney abnormalities. These symptoms can be very severe, and fatal.

Although TTP-like disorders have been associated with various medications, bone marrow transplantation, pregnancy, HIV infection, and autoimmune disease, most cases appear sporadically, without an obvious precipitating factor. This disease is seen most commonly in adults from 20 to 50 years old, with women affected slightly more often than men. In most TTP patients, the onset of the disease occurs in otherwise healthy individuals, and there is no history of a similar condition in other family members. However, in a smaller set of individuals, there is evidence suggesting that the condition may be inherited.

This evidence is rare reported cases of familial TTP, where the disease begins early in life or sometime shortly after birth, with multiple recurrences and thus a chronic relapsing course; other family members may also be affected. The disease strikes about 4 out of every 100,000 people.

Current treatment consists of infusion of fresh frozen plasma with or without plasma exchange or plasmapheresis. In plasmapheresis, blood is withdrawn from the patient as for a blood donation. Then the plasma portion of the blood is removed by passing the blood through a cell separator. The cells are saved, reconstituted with a plasma substitute, and returned to the patient as a blood transfusion. In TTP, this treatment is repeated daily until blood tests show improvement. People who do not respond to this treatment, or who have frequent recurrences, may require removal of the spleen.

Prior to the development of modern treatment protocols, fatality during an acute episode of TTP was greater than 90% (Rock *et al.* [1991] N. Engl. J. Med. *325*, 393-397; George [2000] Blood *96*, 1223-1229). Plasmapheresis has improved the outcome of this disease so that now 80 to 90% of patients recover completely; however, fatalities still occur. Although most incidents of the disease are acute, when relapses occur, the disease can become chronic. Despite marked improvement in treatment outcome, the molecular pathogenesis of TTP is still unknown and the specific plasma factor(s) responsible for the acute onset of this disease, or recovery following treatment, remains to be identified. Because the cause is unknown, there is no way to prevent the disease.

Thus, what is needed are improved methods to treat the disease, to decrease fatality and to decrease the appearance and/or severity of the consequent debilitating symptoms associated with the disease. What is also needed is a method to determine the susceptibility of individuals to the disease, in efforts to prevent the appearance and/or severity of symptoms. What is also needed is a method to identify those individuals for whom the disease appears to be genetic.

SUMMARY OF THE INVENTION

Thus, it is an object of the present invention to provide methods to determine the susceptibility of individuals to TPP, and to identify those individuals for whom the disease appears to be genetic. It is a further object of the present invention to provide improved methods to treat TPP.

These objectives and others are met by the present invention, which in some embodiments provides a method of identifying subjects at risk of developing TTP disease

comprising: providing nucleic acid from a subject, wherein the nucleic acid comprises a *ADAMTS13* gene; and detecting the presence or absence of one or more variations in the *ADAMTS13* gene. In other embodiments, the method further comprises the step of determining if the subject is at risk of developing TTP disease based on the presence or absence of the one or more variations. In yet other embodiments, in the method of the present invention the variation is a single nucleotide polymorphism, or the variation causes a frameshift mutation in *ADAMTS13*, or the variation causes a splice mutation in *ADAMTS13*, or the variation causes a nonconservative amino acid substitution ADAMTS13; preferably, the variation is selected from the group consisting of the mutations shown in Table 1.

In some embodiments, in the method of the present invention, the detecting step is accomplished by hybridization analysis. In further embodiments, the detecting step comprises comparing the sequence of the nucleic acid to the sequence of a wild-type *ADAMTS13* nucleic acid.

The present invention also provides a method of identifying subjects at risk of developing TTP disease comprising: providing a blood sample from a subject, wherein the blood sample comprises an ADAMTS13 protease; and detecting the presence or absence of one or more variants of the ADAMTS13 protease. In some embodiments, the detecting step is accomplished by an antibody assay.

The present invention also provides a kit for determining if a subject is at risk of developing TTP disease comprising a detection assay, wherein the detection assay is capable of specifically detecting a variant *ADAMTS13* allele. In some embodiments, the detection assay comprises a nucleic acid probe that hybridizes under stringent conditions to a nucleic acid sequence comprising at least one mutation selected from the group consisting of the mutations shown in Table 1.

The invention further provides a kit for determining if a subject is at risk of developing TTP disease comprising a detection assay, wherein the detection assay is capable of specifically detecting a variant ADAMTS13 protease. In some embodiments, the detection assay comprises an antibody capable of binding to an ADAMTS13 protease selected from the group consisting of wild-type proteases and proteases comprising at least one amino acid mutation shown in Table 1.

The invention also provides an isolated nucleic acid comprising a sequence encoding a polypeptide selected from the group consisting of SEQ ID NOs: 2 and 4 and variants of SEQ ID NO:2 as shown in Tables 1 and 2. In some embodiments, the sequence is operably

linked to a heterologous promoter. In further embodiments, the invention provides a vector comprising the isolated sequence. In yet further embodiments, the invention provides a host cell comprising the vector. In some embodiments, the host cell is selected from the group consisting of animal and plant cells; in other embodiments, the host cell is located in an organism.

The invention also provides an isolated nucleic acid sequence comprising a sequence selected from the group consisting of SEQ ID NOs: 1 and 3 and variants of SEQ ID NO:1 as shown in Tables 1 and 2. In some embodiments, the invention provides a computer readable medium encoding a representation of the nucleic acid sequence of claim 22.

The invention also provides an isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 2 and 4 and variants of SEQ ID NO:2 as shown in Tables 1 and 2. In some embodiments, the invention provides a computer readable medium encoding a representation of the polypeptide of claim 24. The invention also provides a method of identifying subjects at risk of carrying an allele for TTP disease comprising: providing nucleic acid from a subject, wherein the nucleic acid comprises a *ADAMTS 13* gene; and detecting the presence or absence of one or more variations in the *ADAMTS13* gene. In other embodiments, the method of the present invention further comprises a step of determining if the subject is at risk of carrying TTP disease based on the presence or absence of the one or more variations.

The present invention also provides an isolated nucleic acid comprising a sequence encoding a polypeptide CUB domain of ADAMTS13; preferably, the nucleic acid comprises SEQ ID NO: 5. The present invention also provides an isolated polypeptide comprising a CUB domain of ADAMTS13; preferably, the polypeptide comprises SEQ ID NO: 6.

The present invention also provides a method of treating a patient with TTP disease, comprising administering a therapeutically effective amount of ADAMTS13 protease such that the symptoms of the disease are alleviated, wherein the ADAMTS13 protease is selected from the group consisting: recombinant ADAMTS13; synthetic ADAMTS13; mutants, variants, fragments, and fusions of recombinant ADAMTS13; and mutants, variants, fragments, and fusions of synthetic ADAMTS13.

DESCRIPTION OF THE FIGURES

Figure 1 shows the pedigrees used for linkage analysis. VWF-cleaving protease levels (in U/ml) are indicated beneath the symbol for each individual. Affected individuals are indicated by solid symbols and carriers by dotted symbols. A total of 17 markers as described in Example 1 were used for haplotype analysis. Only select markers are shown. Chromosomes carrying affected alleles are framed, whereas normal chromosomes are not marked. Areas where recombination cannot be definitively assigned are indicated by shading. Only recombination events between affected and unaffected chromosomes are shown. Inferred genotypes are indicated in parentheses. Genotypes of unknown phase are indicated by square brackets. Recombination events in individuals AIII3 and BII6 place the responsible gene below marker GL2-1 and a recombination event in individual AIII2 places the gene above marker D9S1818.

Figure 2 shows blood plasma VWF-cleaving protease levels. Panel **a** shows levels for all individuals shown in Figure 1, as well as additional members of family A. Panel **b** shows levels for 61 normal control individuals. Affected individuals are indicated by circles, obligate carriers (parents of affected individuals) by triangles, other individuals at-risk for inheriting an affected allele by diamonds, and additional not at-risk members of family A by hexagons. Normal controls are shown as triangles. Levels for at-risk individuals (diamonds in panel **a** fall into a bimodal distribution, with one peak ranging from 0.45-0.68 U/ml, consistent with carriers and the other from 0.90-1.17 U/ml, indistinguishable from the normal distribution shown in panel **b**.

Figure 3 shows the identification of the *ADAMTS13* gene. Panel **a** shows a physical map of chromosome 9 in the interval surrounding marker D9S164. The 2.3 Mb nonrecombinant interval identified in Figure 1 is located between the markers that designate this interval, which are shown in larger and bold type. Sequence gaps in public genomic draft assembly (http://genome.ucsc.edu) are denoted by black bars. Transcripts localized to this interval are depicted by black and hatched bars; the different patterns are used solely to make it easier to see the individual transcripts in areas where they are spaced closely together. The predicted gene *C9ORF8* is indicated with an asterisk. The reference bar represents 1 Mb. Panel **b** shows the intron-exon of an *ADAMTS13* gene and the domain structure of the encoded ADAMTS13 protein. The coding regions are indicated by gray bars and the 5' and 3' untranslated regions are indicated by patterned bars. Intron sizes are

not drawn to scale. Exon 1 of *C9ORF8* overlaps with a cluster of EST sequences (Unigene cluster Hs.149184), initially interpreted as predicting a large 5' untranslated region. A segment of putative *C9ORF8* coding sequence was used to identify 2 partial human fetal liver cDNA clones, which were extended in both the 5' and 3' direction by RT-PCR and RACE. The assembled cDNA sequence corrected an error in the predicted boundaries of *C9ORF8* exon 2, resulting in a continuous open reading frame including two exons upstream of the 5' EST cluster, 3 new exons within the predicted intron 10 of *C9ORF8* and 6 additional downstream exons encompassing a second hypothetical gene in this region, *DKFZp434C2322* (Unigene cluster Hs.131433). Analysis of RT-PCR and cDNA sequences identified an alternatively spliced variant of exon 17 using both alternate donor and acceptor splice sites; the alternatively spliced exon pieces are indicated by black bars. Mutations are depicted underneath the corresponding exons, with triangles representing missense mutations and squares representing frameshift and splice mutations. The reference bars represents 200 nucleotides. The predicted domain structure of ADAMTS13 is shown at the bottom of panel **b**. The predicted signal peptide (http://www.cbs.dtu.dk/services/SignalP/) is indicated as "SP," the short propeptide is indicated as "pro," the metalloproteinase domain is indicated by "metalloprotease," the disintegrin domain is indicated by "disintegrin," and TSP1 domains are indicated as ovals. The locations of the zinc-binding catalytic consensus sequence within the metalloproteinase domain and the cysteine rich region within the spacer domain are also indicated. The CUB domain (indicated as "CUB") has not been identified in other ADAMTS family members. The reference bar represents 50 amino acids. Panel **c** shows the domain structure of ADAMTS13, with the locations of mutations indicated. Missense mutations identified in TPP patients are indicated by arrows. The asterisk indicates an additional mutant identified in a TPP family.

Figure 4 shows the results of Northern and RT-PCR analysis of *ADAMTS13*. Panel **a** shows a human Northern blot hybridized with a probe spanning exons 11-13 and part of exon 14. An ~4.7 kb message can be seen specifically in the liver and a truncated, ~2.3 kb message is faintly visible in placenta. Panel **b** shows a panel of cDNAs derived from human tissues screened by PCR for the presence of exons 11-14. Strong signals were seen in the liver and ovary, with weak expression also evident in kidney pancreas, spleen, thymus prostate, testis, intestine and peripheral blood leukocytes. No expression was detected in heart, brain, placenta, lung or muscle.

Figure 5 shows the nucleotide sequence of an *ADAMTS13* cDNA which encodes a long form of ADAMTS13 (SEQ ID NO:1). This sequence includes ambiguity codes for all single nucleotide polymorphisms. The IUPAC ambiguity codes are as follows:

M = A or C

R = A or G

W = A or T

S = C or G

Y = C or T

K = G or T

Figure 6 shows the amino acid sequence of a long form of an ADAMTS13 (SEQ ID NO:2) encoded by the nucleotide sequence of Figure 5. This sequence contains one of the two possible amino acids for regions where Single Nucleotide Polymorphisms (SNPs) change an amino acid; the SNPs and encoded amino acids are shown in Table 2.

Figure 7 shows the nucleotide sequence of an *ADAMTS13* cDNA which encodes a short form of an ADAMTS13 (SEQ ID NO:3). This sequence includes ambiguity codes for all Single Nucleotide Polymorphisms (SNPs). The IUPAC ambiguity codes are as indicated for Figure 5.

Figure 8 shows the amino acid sequence of a short form of ADAMTS13 (SEQ ID NO:4). This sequence contains one of the two possible amino acids for regions where Single Nucleotide Polymorphisms (SNPs) change an amino acid; the SNPs and encoded amino acids are shown in Table 2.

Figure 9 shows the nucleotide sequence (panel a, SEQ ID NO:5) and the amino acid sequence (panel b, SEQ ID NO:6) of an ADAMTS13 CUB domain.

Figure 10 shows the nucleotide sequence of an *ADAMTS13* gene which encodes a wild-type ADAMTS13 (SEQ ID NO:7). This sequence includes ambiguity codes for some Single Nucleotide Polymorphisms (SNPs). The IUPAC ambiguity codes are as indicated for Figure 5.

Figure 11 shows the VWF-cleaving protease activity of ADAMTS13 mutants. VWF-cleaving protease activity was measure in conditioned media of CHO-Tag cells transfected with wild-type (WT) and mutant *ADAMTS13* constructs. Activities are represented as the percentage of the activity of wild-type recombinant ADAMTS13.

DEFINITIONS

To facilitate an understanding of the present invention, a number of terms and phrases as used herein are defined below:

The term "thrombotic thrombocytopenic purpura" or "TTP" refers to a disease characterized by intravascular destruction of erythrocytes and consumption of blood platelets resulting in anemia and thrombocytopenia. Diffuse platelet rich microthrombi are observed in multiple organs, with the major extravascular manifestations including fever, and variable degrees of neurologic and renal dysfunction. Purpura refers to the characteristic bleeding that occurs beneath the skin, or in mucus membranes, which produces bruises, or a red rash-like appearance.

The term "ADAMTS13" refers to a protein encoded by *ADAMTS13*, a gene responsible for familial TTP. *ADAMTS13* has been identified as a unique member of the metalloproteinase gene family, ADAM (a disintegrin and metalloproteinase), whose members are membrane-anchored proteases with diverse functions. ADAMTS family members are distinguished from ADAMs by the presence of one or more thrombospondin 1-like (TSP1) domain(s) at the C-terminus and the absence of the EGF repeat, transmembrane domain and cytoplasmic tail typically observed in ADAM metalloproteinases. It is contemplated that ADAMTS13 possesses VWF (von Wildebrandt factor) cleaving protease activity.

The terms "protein" and "polypeptide" refer to compounds comprising amino acids joined via peptide bonds and are used interchangeably. A "protein" or "polypeptide" encoded by a gene is not limited to the amino acid sequence encoded by the gene, but includes post-translational modifications of the protein.

Where the term "amino acid sequence" is recited herein to refer to an amino acid sequence of a protein molecule, "amino acid sequence" and like terms, such as "polypeptide" or "protein" are not meant to limit the amino acid sequence to the complete, native amino acid sequence associated with the recited protein molecule. Furthermore, an "amino acid sequence" can be deduced from the nucleic acid sequence encoding the protein.

The term "portion" when used in reference to a protein (as in "a portion of a given protein") refers to fragments of that protein. The fragments may range in size from four amino acid residues to the entire amino sequence minus one amino acid.

The term "chimera" when used in reference to a polypeptide refers to the expression product of two or more coding sequences obtained from different genes, that have been

cloned together and that, after translation, act as a single polypeptide sequence. Chimeric polypeptides are also referred to as "hybrid" polypeptides. The coding sequences includes those obtained from the same or from different species of organisms.

The term "fusion" when used in reference to a polypeptide refers to a chimeric protein containing a protein of interest joined to an exogenous protein fragment (the fusion partner). The fusion partner may serve various functions, including enhancement of solubility of the polypeptide of interest, as well as providing an "affinity tag" to allow purification of the recombinant fusion polypeptide from a host cell or from a supernatant or from both. If desired, the fusion partner may be removed from the protein of interest after or during purification.

The term "homolog" or "homologous" when used in reference to a polypeptide refers to a high degree of sequence identity between two polypeptides, or to a high degree of similarity between the three-dimensional structure or to a high degree of similarity between the active site and the mechanism of action. In a preferred embodiment, a homolog has a greater than 60% sequence identity, and more preferably greater than 75% sequence identity, and still more preferably greater than 90% sequence identity, with a reference sequence.

As applied to polypeptides, the term "substantial identity" means that two peptide sequences, when optimally aligned, such as by the programs GAP or BESTFIT using default gap weights, share at least 80 percent sequence identity, preferably at least 90 percent sequence identity, more preferably at least 95 percent sequence identity or more (*e.g.*, 99 percent sequence identity). Preferably, residue positions which are not identical differ by conservative amino acid substitutions.

The terms "variant" and "mutant" when used in reference to a polypeptide refer to an amino acid sequence that differs by one or more amino acids from another, usually related polypeptide. The variant may have "conservative" changes, wherein a substituted amino acid has similar structural or chemical properties. One type of conservative amino acid substitutions refers to the interchangeability of residues having similar side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side

chains is cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, and asparagine-glutamine. More rarely, a variant may have "non-conservative" changes (*e.g.*, replacement of a glycine with a tryptophan). Similar minor variations may also include amino acid deletions or insertions (i.e., additions), or both. Guidance in determining which and how many amino acid residues may be substituted, inserted or deleted without abolishing biological activity may be found using computer programs well known in the art, for example, DNAStar software. Variants can be tested in functional assays. Preferred variants have less than 10%, and preferably less than 5%, and still more preferably less than 2% changes (whether substitutions, deletions, and so on).

The term "domain" when used in reference to a polypeptide refers to a subsection of the polypeptide which possesses a unique structural and/or functional characteristic; typically, this characteristic is similar across diverse polypeptides. The subsection typically comprises contiguous amino acids, although it may also comprise amino acids which act in concert or which are in close proximity due to folding or other configurations. An example of a protein domain is the CUB domain in ADAMTS13, which has been identified in a number of developmentally regulated proteins.

The term "gene" refers to a nucleic acid (*e.g.*, DNA or RNA) sequence that comprises coding sequences necessary for the production of an RNA, or a polypeptide or its precursor (*e.g.*, proinsulin). A functional polypeptide can be encoded by a full length coding sequence or by any portion of the coding sequence as long as the desired activity or functional properties (*e.g.*, enzymatic activity, ligand binding, signal transduction, etc.) of the polypeptide are retained. The term "portion" when used in reference to a gene refers to fragments of that gene. The fragments may range in size from a few nucleotides to the entire gene sequence minus one nucleotide. Thus, "a nucleotide comprising at least a portion of a gene" may comprise fragments of the gene or the entire gene.

The term "gene" also encompasses the coding regions of a structural gene and includes sequences located adjacent to the coding region on both the 5' and 3' ends for a distance of about 1 kb on either end such that the gene corresponds to the length of the full-length mRNA. The sequences which are located 5' of the coding region and which are present on the mRNA are referred to as 5' non-translated sequences. The sequences which are located 3' or downstream of the coding region and which are present on the mRNA are referred to as 3' non-translated sequences. The term "gene" encompasses both cDNA and genomic forms of a gene. A genomic form or clone of a gene contains the coding region

interrupted with non-coding sequences termed "introns" or "intervening regions" or "intervening sequences." Introns are segments of a gene which are transcribed into nuclear RNA (hnRNA); introns may contain regulatory elements such as enhancers. Introns are removed or "spliced out" from the nuclear or primary transcript; introns therefore are absent in the messenger RNA (mRNA) transcript. The mRNA functions during translation to specify the sequence or order of amino acids in a nascent polypeptide.

In addition to containing introns, genomic forms of a gene may also include sequences located on both the 5' and 3' end of the sequences which are present on the RNA transcript. These sequences are referred to as "flanking" sequences or regions (these flanking sequences are located 5' or 3' to the non-translated sequences present on the mRNA transcript). The 5' flanking region may contain regulatory sequences such as promoters and enhancers which control or influence the transcription of the gene. The 3' flanking region may contain sequences which direct the termination of transcription, posttranscriptional cleavage and polyadenylation.

In particular, the term "*ADAMTS13* gene" refers to a full-length *ADAMTS13* nucleotide sequence (*e.g.*, as shown in SEQ ID NO:5). However, it is also intended that the term encompass fragments of the *ADAMTS13* sequence, as well as other domains with the full-length *ADAMTS13* nucleotide sequence. Furthermore, the terms "*ADAMTS 13* nucleotide sequence" or "*ADAMTS13* polynucleotide sequence" encompasses DNA, cDNA, and RNA (*e.g.*, mRNA) sequences.

The term "heterologous" when used in reference to a gene refers to a gene encoding a factor that is not in its natural environment (*i.e.*, has been altered by the hand of man). For example, a heterologous gene includes a gene from one species introduced into another species. A heterologous gene also includes a gene native to an organism that has been altered in some way (*e.*g., mutated, added in multiple copies, linked to a non-native promoter or enhancer sequence, etc.). Heterologous genes may comprise plant gene sequences that comprise cDNA forms of a plant gene; the cDNA sequences may be expressed in either a sense (to produce mRNA) or anti-sense orientation (to produce an anti-sense RNA transcript that is complementary to the mRNA transcript). Heterologous genes are distinguished from endogenous plant genes in that the heterologous gene sequences are typically joined to nucleotide sequences comprising regulatory elements such as promoters that are not found naturally associated with the gene for the protein encoded by the heterologous gene or with plant gene sequences in the chromosome, or are associated with

portions of the chromosome not found in nature (*e.g.*, genes expressed in loci where the gene is not normally expressed).

The term "nucleotide sequence of interest" or "nucleic acid sequence of interest" refers to any nucleotide sequence (*e.g.*, RNA or DNA), the manipulation of which may be deemed desirable for any reason (*e.g.*, treat disease, confer improved qualities, *etc.*), by one of ordinary skill in the art. Such nucleotide sequences include, but are not limited to, coding sequences of structural genes (*e.g.*, reporter genes, selection marker genes, oncogenes, drug resistance genes, growth factors, *etc.*), and non-coding regulatory sequences which do not encode an mRNA or protein product (*e.g.*, promoter sequence, polyadenylation sequence, termination sequence, enhancer sequence, *etc.*).

The term "structural" when used in reference to a gene or to a nucleotide or nucleic acid sequence refers to a gene or a nucleotide or nucleic acid sequence whose ultimate expression product is a protein (such as an enzyme or a structural protein), an rRNA, an sRNA, a tRNA, etc.

The terms "oligonucleotide" or "polynucleotide" or "nucleotide" or "nucleic acid" refer to a molecule comprised of two or more deoxyribonucleotides or ribonucleotides, preferably more than three, and usually more than ten. The exact size will depend on many factors, which in turn depends on the ultimate function or use of the oligonucleotide. The oligonucleotide may be generated in any manner, including chemical synthesis, DNA replication, reverse transcription, or a combination thereof.

The terms "an oligonucleotide having a nucleotide sequence encoding a gene" or "a nucleic acid sequence encoding" a specified polypeptide refer to a nucleic acid sequence comprising the coding region of a gene or in other words the nucleic acid sequence which encodes a gene product. The coding region may be present in either a cDNA, genomic DNA or RNA form. When present in a DNA form, the oligonucleotide may be single-stranded (*i.e.*, the sense strand) or double-stranded. Suitable control elements such as enhancers/promoters, splice junctions, polyadenylation signals, *etc.* may be placed in close proximity to the coding region of the gene if needed to permit proper initiation of transcription and/or correct processing of the primary RNA transcript. Alternatively, the coding region utilized in the expression vectors of the present invention may contain endogenous enhancers/promoters, splice junctions, intervening sequences, polyadenylation signals, *etc.* or a combination of both endogenous and exogenous control elements.

The term "recombinant" when made in reference to a nucleic acid molecule refers to a nucleic acid molecule which is comprised of segments of nucleic acid joined together by

means of molecular biological techniques. The term "recombinant" when made in reference to a protein or a polypeptide refers to a protein molecule which is expressed using a recombinant nucleic acid molecule.

The terms "complementary" and "complementarity" refer to polynucleotides (*i.e.*, a sequence of nucleotides) related by the base-pairing rules. For example, for the sequence "A-G-T," is complementary to the sequence "T-C-A." Complementarity may be "partial," in which only some of the nucleic acids' bases are matched according to the base pairing rules. Or, there may be "complete" or "total" complementarity between the nucleic acids. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of hybridization between nucleic acid strands. This is of particular importance in amplification reactions, as well as detection methods which depend upon binding between nucleic acids.

The term "homology" when used in relation to nucleic acids refers to a degree of complementarity. There may be partial homology or complete homology (*i.e.*, identity). "Sequence identity" refers to a measure of relatedness between two or more nucleic acids or proteins, and is given as a percentage with reference to the total comparison length. The identity calculation takes into account those nucleotide or amino acid residues that are identical and in the same relative positions in their respective larger sequences. Calculations of identity may be performed by algorithms contained within computer programs such as "GAP" (Genetics Computer Group, Madison, Wis.) and "ALIGN" (DNAStar, Madison, Wis.). A partially complementary sequence is one that at least partially inhibits (or competes with) a completely complementary sequence from hybridizing to a target nucleic acid is referred to using the functional term "substantially homologous." The inhibition of hybridization of the completely complementary sequence to the target sequence may be examined using a hybridization assay (Southern or Northern blot, solution hybridization and the like) under conditions of low stringency. A substantially homologous sequence or probe will compete for and inhibit the binding (*i.e.*, the hybridization) of a sequence which is completely homologous to a target under conditions of low stringency. This is not to say that conditions of low stringency are such that non-specific binding is permitted; low stringency conditions require that the binding of two sequences to one another be a specific (*i.e.*, selective) interaction. The absence of non-specific binding may be tested by the use of a second target which lacks even a partial degree of complementarity (*e.g.*, less than about 30% identity); in the absence of non-specific binding the probe will not hybridize to the second non-complementary target.

The following terms are used to describe the sequence relationships between two or more polynucleotides: "reference sequence", "sequence identity", "percentage of sequence identity", and "substantial identity". A "reference sequence" is a defined sequence used as a basis for a sequence comparison; a reference sequence may be a subset of a larger sequence, for example, as a segment of a full-length cDNA sequence given in a sequence listing or may comprise a complete gene sequence. Generally, a reference sequence is at least 20 nucleotides in length, frequently at least 25 nucleotides in length, and often at least 50 nucleotides in length. Since two polynucleotides may each (1) comprise a sequence (*i.e.*, a portion of the complete polynucleotide sequence) that is similar between the two polynucleotides, and (2) may further comprise a sequence that is divergent between the two polynucleotides, sequence comparisons between two (or more) polynucleotides are typically performed by comparing sequences of the two polynucleotides over a "comparison window" to identify and compare local regions of sequence similarity. A "comparison window", as used herein, refers to a conceptual segment of at least 20 contiguous nucleotide positions wherein a polynucleotide sequence may be compared to a reference sequence of at least 20 contiguous nucleotides and wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Optimal alignment of sequences for aligning a comparison window may be conducted by the local homology algorithm of Smith and Waterman (Smith & Waterman [1981] *Adv. Appl. Math.*, 2:482) by the homology alignment algorithm of Needleman and Wunsch (Needleman & Wunsch [1970] *J. Mol. Biol.*, 48:443), by the search for similarity method of Pearson and Lipman (Pearson & Lipman [1988] *Proc. Natl. Acad. Sci. U.S.A.*, 85:2444), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetics Computer Group, 575 Science Dr., Madison, Wis.), or by inspection, and the best alignment (*i.e.*, resulting in the highest percentage of homology over the comparison window) generated by the various methods is selected. The term "sequence identity" means that two polynucleotide sequences are identical (*i.e.*, on a nucleotide-by-nucleotide basis) over the window of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over the window of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, U, or I) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the

window of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The terms "substantial identity" as used herein denotes a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 85 percent sequence identity, preferably at least 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison window of at least 20 nucleotide positions, frequently over a window of at least 25-50 nucleotides, wherein the percentage of sequence identity is calculated by comparing the reference sequence to the polynucleotide sequence which may include deletions or additions which total 20 percent or less of the reference sequence over the window of comparison. The reference sequence may be a subset of a larger sequence, for example, as a segment of the full-length sequences of the compositions claimed in the present invention.

The term "substantially homologous" when used in reference to a double-stranded nucleic acid sequence such as a cDNA or genomic clone refers to any probe that can hybridize to either or both strands of the double-stranded nucleic acid sequence under conditions of low to high stringency as described above.

The term "substantially homologous" when used in reference to a single-stranded nucleic acid sequence refers to any probe that can hybridize (*i.e.*, it is the complement of) the single-stranded nucleic acid sequence under conditions of low to high stringency as described above.

The term "hybridization" refers to the pairing of complementary nucleic acids. Hybridization and the strength of hybridization (*i.e.*, the strength of the association between the nucleic acids) is impacted by such factors as the degree of complementary between the nucleic acids, stringency of the conditions involved, the T_m of the formed hybrid, and the G:C ratio within the nucleic acids. A single molecule that contains pairing of complementary nucleic acids within its structure is said to be "self-hybridized."

The term "T_m" refers to the "melting temperature" of a nucleic acid. The melting temperature is the temperature at which a population of double-stranded nucleic acid molecules becomes half dissociated into single strands. The equation for calculating the T_m of nucleic acids is well known in the art. As indicated by standard references, a simple estimate of the T_m value may be calculated by the equation: $T_m = 81.5 + 0.41(\% G + C)$, when a nucleic acid is in aqueous solution at 1 M NaCl (*See e.g.*, Anderson and Young, Quantitative Filter Hybridization, *in Nucleic Acid Hybridization* [1985]). Other references

include more sophisticated computations that take structural as well as sequence characteristics into account for the calculation of T_m.

The term "stringency" refers to the conditions of temperature, ionic strength, and the presence of other compounds such as organic solvents, under which nucleic acid hybridizations are conducted. With "high stringency" conditions, nucleic acid base pairing will occur only between nucleic acid fragments that have a high frequency of complementary base sequences. Thus, conditions of "low" stringency are often required with nucleic acids that are derived from organisms that are genetically diverse, as the frequency of complementary sequences is usually less.

"Low stringency conditions" when used in reference to nucleic acid hybridization comprise conditions equivalent to binding or hybridization at 42EC in a solution consisting of 5X SSPE (43.8 g/l NaCl, 6.9 g/l $NaH_2PO_4 \bullet H_2O$ and 1.85 g/l EDTA, pH adjusted to 7.4 with NaOH), 0.1% SDS, 5X Denhardt's reagent [50X Denhardt's contains per 500 ml: 5 g Ficoll (Type 400, Pharmacia), 5 g BSA (Fraction V; Sigma)] and 100 μg/ml denatured salmon sperm DNA followed by washing in a solution comprising 5X SSPE, 0.1% SDS at 42EC when a probe of about 500 nucleotides in length is employed.

"Medium stringency conditions" when used in reference to nucleic acid hybridization comprise conditions equivalent to binding or hybridization at 42EC in a solution consisting of 5X SSPE (43.8 g/l NaCl, 6.9 g/l $NaH_2PO_4 \bullet H_2O$ and 1.85 g/l EDTA, pH adjusted to 7.4 with NaOH), 0.5% SDS, 5X Denhardt's reagent and 100 μg/ml denatured salmon sperm DNA followed by washing in a solution comprising 1.0X SSPE, 1.0% SDS at 42EC when a probe of about 500 nucleotides in length is employed.

"High stringency conditions" when used in reference to nucleic acid hybridization comprise conditions equivalent to binding or hybridization at 42EC in a solution consisting of 5X SSPE (43.8 g/l NaCl, 6.9 g/l $NaH_2PO_4 \bullet H_2O$ and 1.85 g/l EDTA, pH adjusted to 7.4 with NaOH), 0.5% SDS, 5X Denhardt's reagent and 100 μg/ml denatured salmon sperm DNA followed by washing in a solution comprising 0.1X SSPE, 1.0% SDS at 42EC when a probe of about 500 nucleotides in length is employed.

It is well known that numerous equivalent conditions may be employed to comprise low stringency conditions; factors such as the length and nature (DNA, RNA, base composition) of the probe and nature of the target (DNA, RNA, base composition, present in solution or immobilized, etc.) and the concentration of the salts and other components (*e.g.*, the presence or absence of formamide, dextran sulfate, polyethylene glycol) are

considered and the hybridization solution may be varied to generate conditions of low stringency hybridization different from, but equivalent to, the above listed conditions. In addition, the art knows conditions that promote hybridization under conditions of high stringency (*e.g.*, increasing the temperature of the hybridization and/or wash steps, the use of formamide in the hybridization solution, etc.).

The term "wild-type" when made in reference to a gene refers to a gene that has the characteristics of a gene isolated from a naturally occurring source. The term "wild-type" when made in reference to a gene product refers to a gene product that has the characteristics of a gene product isolated from a naturally occurring source. The term "naturally-occurring" as applied to an object refers to the fact that an object can be found in nature. For example, a polypeptide or polynucleotide sequence that is present in an organism (including viruses) that can be isolated from a source in nature and which has not been intentionally modified by man in the laboratory is naturally-occurring. A wild-type gene is frequently that gene which is most frequently observed in a population and is thus arbitrarily designated the "normal" or "wild-type" form of the gene. In contrast, the term "modified" or "mutant" when made in reference to a gene or to a gene product refers, respectively, to a gene or to a gene product which displays modifications in sequence and/or functional properties (*i.e.*, altered characteristics) when compared to the wild-type gene or gene product. It is noted that naturally-occurring mutants can be isolated; these are identified by the fact that they have altered characteristics when compared to the wild-type gene or gene product.

Thus, the terms "variant" and "mutant" when used in reference to a nucleotide sequence refer to an nucleic acid sequence that differs by one or more nucleotides from another, usually related nucleotide acid sequence. A "variation" is a difference between two different nucleotide sequences; typically, one sequence is a reference sequence.

The term "polymorphic locus" refers to a genetic locus present in a population that shows variation between members of the population (*i.e.*, the most common allele has a frequency of less than 0.95). Thus, "polymorphism" refers to the existence of a character in two or more variant forms in a population. A "single nucleotide polymorphism" (or SNP) refers a genetic locus of a single base which may be occupied by one of at least two different nucleotides. In contrast, a "monomorphic locus" refers to a genetic locus at which little or no variations are seen between members of the population (generally taken to be a locus at which the most common allele exceeds a frequency of 0.95 in the gene pool of the population).

A "frameshift mutation" refers to a mutation in a nucleotide sequence, usually resulting from insertion or deletion of a single nucleotide (or two or four nucleotides) which results in a change in the correct reading frame of a structural DNA sequence encoding a protein. The altered reading frame usually results in the translated amino-acid sequence being changed or truncated.

A "splice mutation" refers to any mutation that affects gene expression by affecting correct RNA splicing. Splicing mutation may be due to mutations at intron-exon boundaries which alter splice sites.

The term "detection assay" refers to an assay for detecting the presence or absence of a sequence or a variant nucleic acid sequence (*e.g.*, mutation or polymorphism in a given allele of a particular gene, as *e.g.*, *ADAMTS13* gene), or for detecting the presence or absence of a particular protein (*e.g.*, ADAMTS13) or the structure or activity or effect of a particular protein (*e.g.*, VWF-cleaving protease activity) or for detecting the presence or absence of a variant of a particular protein.

The term "hybridization analysis" refers to detection of variant nucleotide sequences in a hybridization assay. In a hybridization assay, the presence of absence of a given single nucleotide polymorphism (SNP) or mutation is determined based on the ability of a nucleotide sequence from the sample to hybridize to a complementary nucleotide molecule (*e.g.*, a oligonucleotide probe). A variety of hybridization assays using a variety of technologies for hybridization and detection are available. A description of a selection of exemplary assays is provided later in the specification, and includes direct detection of hybridization, detection of hybridization using "DNA chip" assays, enzymatic detection of hybridization, and mass spectroscopic assays of hybridization.

The term "antisense" refers to a deoxyribonucleotide sequence whose sequence of deoxyribonucleotide residues is in reverse 5' to 3' orientation in relation to the sequence of deoxyribonucleotide residues in a sense strand of a DNA duplex. A "sense strand" of a DNA duplex refers to a strand in a DNA duplex which is transcribed by a cell in its natural state into a "sense mRNA." Thus an "antisense" sequence is a sequence having the same sequence as the non-coding strand in a DNA duplex. The term "antisense RNA" refers to a RNA transcript that is complementary to all or part of a target primary transcript or mRNA and that blocks the expression of a target gene by interfering with the processing, transport and/or translation of its primary transcript or mRNA. The complementarity of an antisense RNA may be with any part of the specific gene transcript, *i.e.*, at the 5' non-coding sequence, 3' non-coding sequence, introns, or the coding sequence. In addition, as used

herein, antisense RNA may contain regions of ribozyme sequences that increase the efficacy of antisense RNA to block gene expression. "Ribozyme" refers to a catalytic RNA and includes sequence-specific endoribonucleases. "Antisense inhibition" refers to the production of antisense RNA transcripts capable of preventing the expression of the target protein.

"Amplification" is a special case of nucleic acid replication involving template specificity. It is to be contrasted with non-specific template replication (*i.e.*, replication that is template-dependent but not dependent on a specific template). Template specificity is here distinguished from fidelity of replication (*i.e.*, synthesis of the proper polynucleotide sequence) and nucleotide (ribo- or deoxyribo-) specificity. Template specificity is frequently described in terms of "target" specificity. Target sequences are "targets" in the sense that they are sought to be sorted out from other nucleic acid. Amplification techniques have been designed primarily for this sorting out.

Template specificity is achieved in most amplification techniques by the choice of enzyme. Amplification enzymes are enzymes that, under conditions they are used, will process only specific sequences of nucleic acid in a heterogeneous mixture of nucleic acid. For example, in the case of Q_ replicase, MDV-1 RNA is the specific template for the replicase (Kacian *et al.* [1972] Proc. Natl. Acad. Sci. USA, 69:3038). Other nucleic acid will not be replicated by this amplification enzyme. Similarly, in the case of T7 RNA polymerase, this amplification enzyme has a stringent specificity for its own promoters (Chamberlain *et al.* [1970] Nature, 228:227). In the case of T4 DNA ligase, the enzyme will not ligate the two oligonucleotides or polynucleotides, where there is a mismatch between the oligonucleotide or polynucleotide substrate and the template at the ligation junction (Wu & Wallace [1989] Genomics 4:560). Finally, *Taq* and *Pfu* polymerases, by virtue of their ability to function at high temperature, are found to display high specificity for the sequences bounded and thus defined by the primers; the high temperature results in thermodynamic conditions that favor primer hybridization with the target sequences and not hybridization with non-target sequences (H.A. Erlich (ed.), *PCR Technology*, Stockton Press [1989]).

The term "amplifiable nucleic acid" refers to nucleic acids that may be amplified by any amplification method. It is contemplated that "amplifiable nucleic acid" will usually comprise "sample template."

The term "sample template" refers to nucleic acid originating from a sample that is analyzed for the presence of "target" (defined below). In contrast, "background template" is

used in reference to nucleic acid other than sample template that may or may not be present in a sample. Background template is most often inadvertent. It may be the result of carryover, or it may be due to the presence of nucleic acid contaminants sought to be purified away from the sample. For example, nucleic acids from organisms other than those to be detected may be present as background in a test sample.

The term "primer" refers to an oligonucleotide, whether occurring naturally as in a purified restriction digest or produced synthetically, which is capable of acting as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product which is complementary to a nucleic acid strand is induced, (*i.e.*, in the presence of nucleotides and an inducing agent such as DNA polymerase and at a suitable temperature and pH). The primer is preferably single stranded for maximum efficiency in amplification, but may alternatively be double stranded. If double stranded, the primer is first treated to separate its strands before being used to prepare extension products. Preferably, the primer is an oligodeoxyribonucleotide. The primer must be sufficiently long to prime the synthesis of extension products in the presence of the inducing agent. The exact lengths of the primers will depend on many factors, including temperature, source of primer and the use of the method.

The term "probe" refers to an oligonucleotide (*i.e.*, a sequence of nucleotides), whether occurring naturally as in a purified restriction digest or produced synthetically, recombinantly or by PCR amplification, that is capable of hybridizing to another oligonucleotide of interest. A probe may be single-stranded or double-stranded. Probes are useful in the detection, identification and isolation of particular gene sequences. It is contemplated that any probe used in the present invention will be labeled with any "reporter molecule," so that is detectable in any detection system, including, but not limited to enzyme (*e.g.*, ELISA, as well as enzyme-based histochemical assays), fluorescent, radioactive, and luminescent systems. It is not intended that the present invention be limited to any particular detection system or label.

The term "target," when used in reference to the polymerase chain reaction, refers to the region of nucleic acid bounded by the primers used for polymerase chain reaction. Thus, the "target" is sought to be sorted out from other nucleic acid sequences. A "segment" is defined as a region of nucleic acid within the target sequence.

The term "polymerase chain reaction" ("PCR") refers to the method of K.B. Mullis U.S. Patent Nos. 4,683,195, 4,683,202, and 4,965,188, that describe a method for increasing the concentration of a segment of a target sequence in a mixture of genomic DNA without

cloning or purification. This process for amplifying the target sequence consists of introducing a large excess of two oligonucleotide primers to the DNA mixture containing the desired target sequence, followed by a precise sequence of thermal cycling in the presence of a DNA polymerase. The two primers are complementary to their respective strands of the double stranded target sequence. To effect amplification, the mixture is denatured and the primers then annealed to their complementary sequences within the target molecule. Following annealing, the primers are extended with a polymerase so as to form a new pair of complementary strands. The steps of denaturation, primer annealing, and polymerase extension can be repeated many times (*i.e.*, denaturation, annealing and extension constitute one "cycle"; there can be numerous "cycles") to obtain a high concentration of an amplified segment of the desired target sequence. The length of the amplified segment of the desired target sequence is determined by the relative positions of the primers with respect to each other, and therefore, this length is a controllable parameter. By virtue of the repeating aspect of the process, the method is referred to as the "polymerase chain reaction" (hereinafter "PCR"). Because the desired amplified segments of the target sequence become the predominant sequences (in terms of concentration) in the mixture, they are said to be "PCR amplified."

With PCR, it is possible to amplify a single copy of a specific target sequence in genomic DNA to a level detectable by several different methodologies (*e.g.*, hybridization with a labeled probe; incorporation of biotinylated primers followed by avidin-enzyme conjugate detection; incorporation of ^{32}P-labeled deoxynucleotide triphosphates, such as dCTP or dATP, into the amplified segment). In addition to genomic DNA, any oligonucleotide or polynucleotide sequence can be amplified with the appropriate set of primer molecules. In particular, the amplified segments created by the PCR process itself are, themselves, efficient templates for subsequent PCR amplifications.

The terms "PCR product," "PCR fragment," and "amplification product" refer to the resultant mixture of compounds after two or more cycles of the PCR steps of denaturation, annealing and extension are complete. These terms encompass the case where there has been amplification of one or more segments of one or more target sequences.

The term "amplification reagents" refers to those reagents (deoxyribonucleotide triphosphates, buffer, etc.), needed for amplification except for primers, nucleic acid template, and the amplification enzyme. Typically, amplification reagents along with other reaction components are placed and contained in a reaction vessel (test tube, microwell, etc.).

The term "reverse-transcriptase" or "RT-PCR" refers to a type of PCR where the starting material is mRNA. The starting mRNA is enzymatically converted to complementary DNA or "cDNA" using a reverse transcriptase enzyme. The cDNA is then used as a "template" for a "PCR" reaction

The term "gene expression" refers to the process of converting genetic information encoded in a gene into RNA (*e.g.*, mRNA, rRNA, tRNA, or snRNA) through "transcription" of the gene (*i.e.*, via the enzymatic action of an RNA polymerase), and into protein, through "translation" of mRNA. Gene expression can be regulated at many stages in the process. "Up-regulation" or "activation" refers to regulation that increases the production of gene expression products (*i.e.*, RNA or protein), while "down-regulation" or "repression" refers to regulation that decrease production. Molecules (*e.g.*, transcription factors) that are involved in up-regulation or down-regulation are often called "activators" and "repressors," respectively.

The terms "in operable combination", "in operable order" and "operably linked" refer to the linkage of nucleic acid sequences in such a manner that a nucleic acid molecule capable of directing the transcription of a given gene and/or the synthesis of a desired protein molecule is produced. The term also refers to the linkage of amino acid sequences in such a manner so that a functional protein is produced.

The term "regulatory element" refers to a genetic element which controls some aspect of the expression of nucleic acid sequences. For example, a promoter is a regulatory element which facilitates the initiation of transcription of an operably linked coding region. Other regulatory elements are splicing signals, polyadenylation signals, termination signals, *etc.*

Transcriptional control signals in eukaryotes comprise "promoter" and "enhancer" elements. Promoters and enhancers consist of short arrays of DNA sequences that interact specifically with cellular proteins involved in transcription (Maniatis, *et al.* [1987] Science 236:1237). Promoter and enhancer elements have been isolated from a variety of eukaryotic sources including genes in yeast, insect, mammalian and plant cells. Promoter and enhancer elements have also been isolated from viruses and analogous control elements, such as promoters, are also found in prokaryotes. The selection of a particular promoter and enhancer depends on the cell type used to express the protein of interest. Some eukaryotic promoters and enhancers have a broad host range while others are functional in a limited subset of cell types (*for review, see* Voss, *et al.*, Trends Biochem. Sci., 11:287, 1986; and Maniatis, *et al.*, *supra* 1987).

The terms "promoter element," "promoter," or "promoter sequence" refer to a DNA sequence that is located at the 5' end (*i.e.* precedes) of the coding region of a DNA polymer. The location of most promoters known in nature precedes the transcribed region. The promoter functions as a switch, activating the expression of a gene. If the gene is activated, it is said to be transcribed, or participating in transcription. Transcription involves the synthesis of mRNA from the gene. The promoter, therefore, serves as a transcriptional regulatory element and also provides a site for initiation of transcription of the gene into mRNA.

The term "regulatory region" refers to a gene's 5' transcribed but untranslated regions, located immediately downstream from the promoter and ending just prior to the translational start of the gene.

The term "promoter region" refers to the region immediately upstream of the coding region of a DNA polymer, and is typically between about 500 bp and 4 kb in length, and is preferably about 1 to 1.5 kb in length.

Promoters may be tissue specific or cell specific. The term "tissue specific" as it applies to a promoter refers to a promoter that is capable of directing selective expression of a nucleotide sequence of interest to a specific type of tissue (*e.g.*, seeds) in the relative absence of expression of the same nucleotide sequence of interest in a different type of tissue (*e.g.*, leaves). Tissue specificity of a promoter may be evaluated by, for example, operably linking a reporter gene to the promoter sequence to generate a reporter construct, introducing the reporter construct into the genome of a plant such that the reporter construct is integrated into every tissue of the resulting transgenic plant, and detecting the expression of the reporter gene (*e.g.*, detecting mRNA, protein, or the activity of a protein encoded by the reporter gene) in different tissues of the transgenic plant. The detection of a greater level of expression of the reporter gene in one or more tissues relative to the level of expression of the reporter gene in other tissues shows that the promoter is specific for the tissues in which greater levels of expression are detected. The term "cell type specific" as applied to a promoter refers to a promoter which is capable of directing selective expression of a nucleotide sequence of interest in a specific type of cell in the relative absence of expression of the same nucleotide sequence of interest in a different type of cell within the same tissue. The term "cell type specific" when applied to a promoter also means a promoter capable of promoting selective expression of a nucleotide sequence of interest in a region within a single tissue. Cell type specificity of a promoter may be assessed using methods well known in the art, *e.g.*, immunohistochemical staining. Briefly, tissue sections

are embedded in paraffin, and paraffin sections are reacted with a primary antibody which is specific for the polypeptide product encoded by the nucleotide sequence of interest whose expression is controlled by the promoter. A labeled (*e.g.*, peroxidase conjugated) secondary antibody which is specific for the primary antibody is allowed to bind to the sectioned tissue and specific binding detected (*e.g.*, with avidin/biotin) by microscopy.

Promoters may be constitutive or inducible. The term "constitutive" when made in reference to a promoter means that the promoter is capable of directing transcription of an operably linked nucleic acid sequence in the absence of a stimulus (*e.g.*, heat shock, chemicals, light, *etc.*). Typically, constitutive promoters are capable of directing expression of a transgene in substantially any cell and any tissue. Exemplary constitutive plant promoters include, but are not limited to SD Cauliflower Mosaic Virus (CaMV SD; *see e.g.*, U.S. Pat. No. 5,352,605, incorporated herein by reference), mannopine synthase, octopine synthase (ocs), superpromoter (*see e.g.*, WO 95/14098), and *ubi3* (*see e.g.*, Garbarino and Belknap, Plant Mol. Biol. 24:119-127 [1994]) promoters. Such promoters have been used successfully to direct the expression of heterologous nucleic acid sequences in transformed plant tissue.

In contrast, an "inducible" promoter is one which is capable of directing a level of transcription of an operably linked nucleic acid sequence in the presence of a stimulus (*e.g.*, heat shock, chemicals, light, *etc.*) which is different from the level of transcription of the operably linked nucleic acid sequence in the absence of the stimulus.

The term "regulatory element" refers to a genetic element that controls some aspect of the expression of nucleic acid sequence(s). For example, a promoter is a regulatory element that facilitates the initiation of transcription of an operably linked coding region. Other regulatory elements are splicing signals, polyadenylation signals, termination signals, etc.

The enhancer and/or promoter may be "endogenous" or "exogenous" or "heterologous." An "endogenous" enhancer or promoter is one that is naturally linked with a given gene in the genome. An "exogenous" or "heterologous" enhancer or promoter is one that is placed in juxtaposition to a gene by means of genetic manipulation (*i.e.*, molecular biological techniques) such that transcription of the gene is directed by the linked enhancer or promoter. For example, an endogenous promoter in operable combination with a first gene can be isolated, removed, and placed in operable combination with a second gene, thereby making it a "heterologous promoter" in operable combination with the second

gene. A variety of such combinations are contemplated (*e.g.*, the first and second genes can be from the same species, or from different species).

The term "naturally linked" or "naturally located" when used in reference to the relative positions of nucleic acid sequences means that the nucleic acid sequences exist in nature in the relative positions.

The presence of "splicing signals" on an expression vector often results in higher levels of expression of the recombinant transcript in eukaryotic host cells. Splicing signals mediate the removal of introns from the primary RNA transcript and consist of a splice donor and acceptor site (Sambrook, *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory Press, New York [1989] pp. 16.7-16.8). A commonly used splice donor and acceptor site is the splice junction from the 16S RNA of SV40.

Efficient expression of recombinant DNA sequences in eukaryotic cells requires expression of signals directing the efficient termination and polyadenylation of the resulting transcript. Transcription termination signals are generally found downstream of the polyadenylation signal and are a few hundred nucleotides in length. The term "poly(A) site" or "poly(A) sequence" as used herein denotes a DNA sequence which directs both the termination and polyadenylation of the nascent RNA transcript. Efficient polyadenylation of the recombinant transcript is desirable, as transcripts lacking a poly(A) tail are unstable and are rapidly degraded. The poly(A) signal utilized in an expression vector may be "heterologous" or "endogenous." An endogenous poly(A) signal is one that is found naturally at the 3' end of the coding region of a given gene in the genome. A heterologous poly(A) signal is one which has been isolated from one gene and positioned 3' to another gene. A commonly used heterologous poly(A) signal is the SV40 poly(A) signal. The SV40 poly(A) signal is contained on a 237 bp *Bam*HI/*Bcl*I restriction fragment and directs both termination and polyadenylation (Sambrook, *supra*, at 16.6-16.7).

The term "vector" refers to nucleic acid molecules that transfer DNA segment(s) from one cell to another. The term "vehicle" is sometimes used interchangeably with "vector."

The terms "expression vector" or "expression cassette" refer to a recombinant DNA molecule containing a desired coding sequence and appropriate nucleic acid sequences necessary for the expression of the operably linked coding sequence in a particular host organism. Nucleic acid sequences necessary for expression in prokaryotes usually include a promoter, an operator (optional), and a ribosome binding site, often along with other

sequences. Eukaryotic cells are known to utilize promoters, enhancers, and termination and polyadenylation signals.

The term "transfection" refers to the introduction of foreign DNA into cells. Transfection may be accomplished by a variety of means known to the art including calcium phosphate-DNA co-precipitation, DEAE-dextran-mediated transfection, polybrene-mediated transfection, glass beads, electroporation, microinjection, liposome fusion, lipofection, protoplast fusion, viral infection, biolistics (*i.e.*, particle bombardment) and the like.

The term "stable transfection" or "stably transfected" refers to the introduction and integration of foreign DNA into the genome of the transfected cell. The term "stable transfectant" refers to a cell that has stably integrated foreign DNA into the genomic DNA.

The term "transient transfection" or "transiently transfected" refers to the introduction of foreign DNA into a cell where the foreign DNA fails to integrate into the genome of the transfected cell. The foreign DNA persists in the nucleus of the transfected cell for several days. During this time the foreign DNA is subject to the regulatory controls that govern the expression of endogenous genes in the chromosomes. The term "transient transfectant" refers to cells that have taken up foreign DNA but have failed to integrate this DNA.

The term "calcium phosphate co-precipitation" refers to a technique for the introduction of nucleic acids into a cell. The uptake of nucleic acids by cells is enhanced when the nucleic acid is presented as a calcium phosphate-nucleic acid co-precipitate. The original technique of Graham and van der Eb (Graham & van der Eb [1973] Virol., 52:456), has been modified by several groups to optimize conditions for particular types of cells. The art is well aware of these numerous modifications.

The terms "infecting" and "infection" when used with a bacterium refer to co-incubation of a target biological sample, (*e.g.*, cell, tissue, *etc.*) with the bacterium under conditions such that nucleic acid sequences contained within the bacterium are introduced into one or more cells of the target biological sample.

The terms "bombarding, "bombardment," and "biolistic bombardment" refer to the process of accelerating particles towards a target biological sample (*e.g.*, cell, tissue, *etc.*) to effect wounding of the cell membrane of a cell in the target biological sample and/or entry of the particles into the target biological sample. Methods for biolistic bombardment are known in the art (*e.g.*, U.S. Patent No. 5,584,807, the contents of which are incorporated

herein by reference), and are commercially available (*e.g.*, the helium gas-driven microprojectile accelerator (PDS-1000/He, BioRad).

The term "transgene" refers to a foreign gene that is placed into an organism by the process of transfection. The term "foreign gene" refers to any nucleic acid (*e.g.*, gene sequence) that is introduced into the genome of an organism by experimental manipulations and may include gene sequences found in that organism so long as the introduced gene does not reside in the same location as does the naturally-occurring gene.

The term "transgenic" when used in reference to a host cell or an organism refers to a host cell or an organism that contains at least one heterologous or foreign gene in the host cell or in one or more of cells of the organism.

The term "host cell" refers to any cell capable of replicating and/or transcribing and/or translating a heterologous gene. Thus, a "host cell" refers to any eukaryotic or prokaryotic cell (*e.g.*, bacterial cells such as *E. coli*, yeast cells, mammalian cells, avian cells, amphibian cells, plant cells, fish cells, and insect cells), whether located *in vitro* or *in vivo*. For example, host cells may be located in a transgenic animal.

The terms "transformants" or "transformed cells" include the primary transformed cell and cultures derived from that cell without regard to the number of transfers. All progeny may not be precisely identical in DNA content, due to deliberate or inadvertent mutations. Mutant progeny that have the same functionality as screened for in the originally transformed cell are included in the definition of transformants.

The term "selectable marker" refers to a gene which encodes an enzyme having an activity that confers resistance to an antibiotic or drug upon the cell in which the selectable marker is expressed, or which confers expression of a trait which can be detected (*e.g.*., luminescence or fluorescence). Selectable markers may be "positive" or "negative." Examples of positive selectable markers include the neomycin phosphotrasferase (NPTII) gene which confers resistance to G418 and to kanamycin, and the bacterial hygromycin phosphotransferase gene (*hyg*), which confers resistance to the antibiotic hygromycin. Negative selectable markers encode an enzymatic activity whose expression is cytotoxic to the cell when grown in an appropriate selective medium. For example, the HSV-*tk* gene is commonly used as a negative selectable marker. Expression of the HSV-*tk* gene in cells grown in the presence of gancyclovir or acyclovir is cytotoxic; thus, growth of cells in selective medium containing gancyclovir or acyclovir selects against cells capable of expressing a functional HSV TK enzyme.

The term "reporter gene" refers to a gene encoding a protein that may be assayed. Examples of reporter genes include, but are not limited to, luciferase (*See, e.g.*, deWet *et al.*, Mol. Cell. Biol. 7:725 [1987] and U.S. Pat Nos.,6,074,859; 5,976,796; 5,674,713; and 5,618,682; all of which are incorporated herein by reference), green fluorescent protein (*e.g.*, GenBank Accession Number U43284; a number of GFP variants are commercially available from CLONTECH Laboratories, Palo Alto, CA), chloramphenicol acetyltransferase, β-galactosidase, alkaline phosphatase, and horse radish peroxidase.

The term "overexpression" refers to the production of a gene product in transgenic organisms that exceeds levels of production in normal or non-transformed organisms. The term "cosuppression" refers to the expression of a foreign gene which has substantial homology to an endogenous gene resulting in the suppression of expression of both the foreign and the endogenous gene. As used herein, the term "altered levels" refers to the production of gene product(s) in transgenic organisms in amounts or proportions that differ from that of normal or non-transformed organisms.

The terms "Southern blot analysis" and "Southern blot" and "Southern" refer to the analysis of DNA on agarose or acrylamide gels in which DNA is separated or fragmented according to size followed by transfer of the DNA from the gel to a solid support, such as nitrocellulose or a nylon membrane. The immobilized DNA is then exposed to a labeled probe to detect DNA species complementary to the probe used. The DNA may be cleaved with restriction enzymes prior to electrophoresis. Following electrophoresis, the DNA may be partially depurinated and denatured prior to or during transfer to the solid support. Southern blots are a standard tool of molecular biologists (J. Sambrook *et al.* [1989] *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press, NY, pp 9.31-9.58).

The term "Northern blot analysis" and "Northern blot" and "Northern" refer to the analysis of RNA by electrophoresis of RNA on agarose gels to fractionate the RNA according to size followed by transfer of the RNA from the gel to a solid support, such as nitrocellulose or a nylon membrane. The immobilized RNA is then probed with a labeled probe to detect RNA species complementary to the probe used. Northern blots are a standard tool of molecular biologists (J. Sambrook, *et al.* [1989] *supra*, pp 7.39-7.52).

The terms "Western blot analysis" and "Western blot" and "Western" refers to the analysis of protein(s) (or polypeptides) immobilized onto a support such as nitrocellulose or a membrane. A mixture comprising at least one protein is first separated on an acrylamide gel, and the separated proteins are then transferred from the gel to a solid support, such as nitrocellulose or a nylon membrane. The immobilized proteins are exposed to at least one

antibody with reactivity against at least one antigen of interest. The bound antibodies may be detected by various methods, including the use of radiolabeled antibodies.

The term "antigenic determinant" refers to that portion of an antigen that makes contact with a particular antibody (*i.e.*, an epitope). When a protein or fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies that bind specifically to a given region or three-dimensional structure on the protein; these regions or structures are referred to as antigenic determinants. An antigenic determinant may compete with the intact antigen (*i.e.*, the "immunogen" used to elicit the immune response) for binding to an antibody.

The term "isolated" when used in relation to a nucleic acid, as in "an isolated oligonucleotide" refers to a nucleic acid sequence that is identified and separated from at least one contaminant nucleic acid with which it is ordinarily associated in its natural source. Isolated nucleic acid is present in a form or setting that is different from that in which it is found in nature. In contrast, non-isolated nucleic acids, such as DNA and RNA, are found in the state they exist in nature. Examples of non-isolated nucleic acids include: a given DNA sequence (*e.*g., a gene) found on the host cell chromosome in proximity to neighboring genes; RNA sequences, such as a specific mRNA sequence encoding a specific protein, found in the cell as a mixture with numerous other mRNAs which encode a multitude of proteins. However, isolated nucleic acid encoding a particular protein includes, by way of example, such nucleic acid in cells ordinarily expressing the protein, where the nucleic acid is in a chromosomal location different from that of natural cells, or is otherwise flanked by a different nucleic acid sequence than that found in nature. The isolated nucleic acid or oligonucleotide may be present in single-stranded or double-stranded form. When an isolated nucleic acid or oligonucleotide is to be utilized to express a protein, the oligonucleotide will contain at a minimum the sense or coding strand (*i.e.*, the oligonucleotide may single-stranded), but may contain both the sense and anti-sense strands (*i.e.*, the oligonucleotide may be double-stranded).

The term "purified" refers to molecules, either nucleic or amino acid sequences, that are removed from their natural environment, isolated or separated. An "isolated nucleic acid sequence" may therefore be a purified nucleic acid sequence. "Substantially purified" molecules are at least 60% free, preferably at least 75% free, and more preferably at least 90% free from other components with which they are naturally associated. As used herein, the term "purified" or "to purify" also refer to the removal of contaminants from a sample. The removal of contaminating proteins results in an increase in the percent of polypeptide

of interest in the sample. In another example, recombinant polypeptides are expressed in plant, bacterial, yeast, or mammalian host cells and the polypeptides are purified by the removal of host cell proteins; the percent of recombinant polypeptides is thereby increased in the sample.

The term "composition comprising" a given polynucleotide sequence or polypeptide refers broadly to any composition containing the given polynucleotide sequence or polypeptide. The composition may comprise an aqueous solution. Compositions comprising polynucleotide sequences encoding ADAMTS13 (*e.g.*, SEQ ID NO:2) or fragments thereof may be employed as hybridization probes. In this case, the ADAMTS13 encoding polynucleotide sequences are typically employed in an aqueous solution containing salts (*e.g.*, NaCl), detergents (*e.g.*, SDS), and other components (*e.g.*, Denhardt's solution, dry milk, salmon sperm DNA, etc.).

The term "test compound" refers to any chemical entity, pharmaceutical, drug, and the like that can be used to treat or prevent a disease, illness, sickness, or disorder of bodily function, or otherwise alter the physiological or cellular status of a sample. Test compounds comprise both known and potential therapeutic compounds. A test compound can be determined to be therapeutic by screening using the screening methods of the present invention. A "known therapeutic compound" refers to a therapeutic compound that has been shown (*e.g.*, through animal trials or prior experience with administration to humans) to be effective in such treatment or prevention.

As used herein, the term "response," when used in reference to an assay, refers to the generation of a detectable signal (*e.g.*, accumulation of reporter protein, increase in ion concentration, accumulation of a detectable chemical product).

The term "sample" is used in its broadest sense. In one sense it can refer to a plant cell or tissue. In another sense, it is meant to include a specimen or culture obtained from any source, as well as biological and environmental samples. Biological samples may be obtained from plants or animals (including humans) and encompass fluids, solids, tissues, and gases. Environmental samples include environmental material such as surface matter, soil, water, and industrial samples. These examples are not to be construed as limiting the sample types applicable to the present invention.

GENERAL DESCRIPTION OF THE INVENTION

Although the cause of TTP is unknown, some evidence suggested that the treatment resulted from removal of a toxic factor from the blood, while other evidence suggested that it replaced a missing factor. Recent evidence suggested that the missing factor could be a type of protein called a protease, and in particular a protease which degrades another blood clotting factor called von Willebrand factor (VWF). In 1982, Moake *et al* (Moake *et al.* [1982] N. Engl. J. Med. *307*, 1432-1435) observed unusually large multimeric forms of von Willebrand factor (VWF) in the plasma of TTP patients and postulated that these patients may lack an activity that is responsible for decreasing the size of VWF secreted from endothelial cells. In 1996, two groups independently isolated a protease from plasma that appears to be responsible for the physiologic cleavage of VWF at the Tyr842-Met843 peptide bond, producing the characteristic 176 kd and 140 kd proteolytic fragments observed in normal plasma (Tsai, H.M. [1996] Blood *87*, 4235-4244; Furlan *et al.* [1996] Blood *87*, 4223-4234). Increased susceptibility to this proteolytic cleavage appears to be responsible for the loss of large VWF multimers central to the pathophysiology of a different disease, type 2A von Willebrand disease (VWD) (Tsai *et al.* [1997] Blood *89*, 1954-1962). The same protease activity was subsequently shown to be deficient in the plasma of TTP patients (Tsai and Lian [1998] N. Engl. J. Med. *339*, 1585-1594; Furlan *et al.* [1998] N. Engl. J. Med. *339*, 1578-1584). The hypothesis that the disease results from the presence of a toxic factor in the blood is supported by reports of circulating autoantibodies detected in most adults with disease (Tsai and Lian [1998] N. Engl. J. Med. *339*, 1585-1594; Furlan *et al.* [1998] N. Engl. J. Med. *339*, 1578-1584), as well as recent reports of antibodies against this protease which been identified in a form of TTP associated with the antiplatelet drug ticlopidine(Tsai *et al.* [2000] Ann. Intern. Med. *132*, 794-799).

Despite the strong association of low VWF-cleaving protease activity with TTP, a direct causative link has not yet been established. Other studies have implicated platelet aggregating proteins or endothelial injury as the underlying mechanism (Mitra *et al.* [1997] Blood *89*, 1224-1234); Dang *et al.* [1999] Blood *93*, 1264-1270; Cines *et al.* [2000] Thromb. Haemost. *84*, 528-535) and enhanced rather than decreased VWF proteolysis has been observed in some patients (Mannucci *et al.* [1989] Blood *74*, 978-983]. Though the protease responsible for VWF cleavage has been partially purified and characterized (Tsai *et al.* [1997] Blood *89*, 1954-1962; Furlan *et al.* [1996] Blood *87*, 4223-4234), it appears to

be present at relatively low levels in plasma and its identification at the sequence level has remained elusive.

The present invention provides identification and characterization of the gene responsible for familial TTP. This was accomplished by studying a series of families in which TTP appears to be inherited and then using a positional cloning approach to map a gene responsible for reduced VWF-cleaving protease activity to a locus on 9q34. The gene was identified as *ADAMTS13* which encodes ADAMTS13, a unique member of the metalloproteinase gene family. Expression of ADAMTS13 from cloned full-length cDNA confirmed its VWF-cleaving protease activity. At least two different forms of ADAMTS13 have been identified, which vary in length. Moreover, mutations in this gene were discovered in individuals affected with TTP. All but 3 of 13 *ADAMTS13* mutations identified were missense mutations. Moreover, the two frameshift and one splice mutations identified were present in trans with a missense mutation on the other allele, which suggests that complete deficiency of ADAMTS13 may be lethal. Nine TTP-related *ADAMTS13* missense mutations severely impair VWF-cleaving protease activity, accounting for the loss of activity observed in the corresponding patient plasmas.

Thus, the present invention provides nucleotide sequences encoding wild-type, mutants, variants, and fragments of ADAMTS13, as well as the encoded proteins. The present invention further provides methods of using the *ADAMTS13* gene and protein, which include but are not limited to precise and rapid diagnosis of this condition in other individuals with inherited TTP, such as with nucleic acid probes or with antibodies, treatment of patients with TTP with a recombinant ADAMTS13, and treatment of patients at risk of or suffering from heart attack or stroke with this protease or other drugs developed from this protease which act as anticoagulants.

In the following description of the discovery and characterization of the *ADAMTS13* gene, mutants, and variants, hypotheses may be advanced to explain certain results, or to correlate results with previous observations. It is not necessary to understand the mechanism underlying the invention, nor is it intended that the invention be limited to any particular mechanism.

A. Discovery of the *ADAMTS13* Gene

1. Analysis of Plasma Level of VWF-Cleaving Protease.

Four pedigrees of families in which TTP appears to be inherited were available for analysis, and are shown in Figure 1. The levels of plasma VWF-cleaving protease were

analyzed as described in Example 1B; the results indicated that the plasma level of VWF-cleaving protease segregated as a semidominant autosomal trait.

VWF-cleaving protease activity measured in the plasma of the 7 affected individuals ranged from 2-7% of normal (0.02 - 0.07 U/ml) and none of the patients tested positive for inhibitors of the protease. Plasma protease levels in the parents of the affected individuals ranged from 0.51-0.68 U/ml, consistent with a heterozygous carrier state. Similarly, levels for at-risk siblings of the patients and parents fell into a bimodal distribution, with one peak consistent with carriers and the other indistinguishable from the normal distribution (Figure 2). These results demonstrate that the protease activity assay used here reliably distinguishes between normal and carrier individuals in these families. This observation suggested that the plasma level of VWF-cleaving protease could be used as a phenotypic trait for linkage analysis to map the corresponding locus, providing considerably greater genetic power than would be available from analysis of the clinical phenotype alone.

2. Mapping the Gene for Familial TTP to Chromosome 9q34.

A genome wide linkage scan was thus performed on the four pedigrees shown in Figure 1 using 382 polymorphic microsatellite markers to analyze DNA from affected individuals and other informative family members, as described in Example 1. Two-point linkage analysis using a recessive model gave a maximum LOD score of 2.36 at $\theta = 0.0$ for marker D9S164 on chromosome 9q34, with a LOD score of 3.83 at $\theta = 0.01$ for a codominant model. Multipoint analysis for D9S164 and 4 flanking markers (cen-D9S1682-D9S290-D95164-D9S1826-D9S158-tel) yielded a maximum LOD score of 4.77 at a location 2.4 cM telomeric to marker D9S164. Genotypes for 7 other markers in this region (Dib, C. *et al.* [1996] Nature *380*, 152-154;. Broman, K.W. *et al.* [1998] Am. J. Hum. Genet. *63*, 861-869) allowed the gene to be placed in the ~7 cM interval between markers D9S1863 and D9S1818 (Figures 1 and 3A). Analysis of additional polymorphic markers (see Table 3 in Example 1) designed from simple sequence repeat data available from the Human Genome Working Draft (http://genome.ucsc.edu) narrowed the candidate interval to an ~2.3 Mb genomic segment between markers GL2-1 and D9S1818. In all but one case, carrier status as determined by haplotype analysis was consistent with the phenotypic designation according to plasma protease level. The exception, individual II2 in pedigree A, shares the affected haplotype of her brother (II4), but has a protease level of 0.8 U/ml, which is borderline between the normal and carrier ranges.

3. Identification of a Candidate Gene for Familial TTP.

Analysis of the candidate interval using public genome database resources (http://genome.ucsc.edu, http://www.ncbi.nlm.nih.gov/) identified ~20 known or predicted genes (Figure 3A). Initial attention focused on genes likely to encode a protease or protease cofactor. *FCN2* (*ficolin 2*) mapped to distal chromosome 9 but could not be identified in available BAC sequence from the candidate interval. However, in light of previous reports suggesting a protease associated function for some ficolin family members (Matsushita,M. & Fujita,T. Ficolins [2001] Immunol. Rev. *180*, 78-85) and the possibility that *FCN2* might lie in one of the three large genomic sequence gaps shown in Figure 3A, the coding exons and intron/exon boundaries of this gene were amplified by PCR from patient DNA and subjected to sequence analysis. No candidate mutations were identified. Two putative genes in the candidate interval, *KIAA0605*, an uncharacterized EST from a brain cDNA library (Nagase, T. *et al.* [1998] DNA Res. *5*, 31-39), and the predicted open reading frame *C9ORF8*, exhibited homology to the ADAMTS family of metalloproteinases, but appeared to lack the conserved protease catalytic domain. Partial DNA sequence analysis of exons and flanking intron sequences failed to identify any mutations in *KIAA0605*. However, the identification of several candidate missense mutations in the predicted exons of *C9ORF8* led to further, more detailed analysis of this candidate gene.

Exon 1 of *C9ORF8* overlapped with a cluster of EST sequences (Unigene cluster Hs.149184), predicting a large 5' untranslated region. A segment of putative *C9ORF8* coding sequence was used to probe a human fetal cDNA library identifying several partial cDNA clones, which were extended in both the 5' and 3' direction by RT-PCR and RACE. The assembled cDNA sequence corrected an error in the predicted boundaries of *C9ORF8* exon 2, resulting in a continuous open reading frame including two exons upstream of the 5' EST cluster, 3 new exons within the predicted intron 10 of *C9ORF8* and 6 additional downstream exons overlapping a second hypothetical gene in this region, *DKFZp434C2322* (Unigene cluster Hs.131433). Thus, through a combination of cDNA cloning, RACE, and genomic sequence analysis, the full length cDNA sequence (Figure 5) and corresponding genomic structure were deduced, as depicted in Figure 3B, and found to encode a complete, potentially catalytically active ADAMTS protease (Figure 6). This gene was discovered to be a novel member of the ADAMTS family of metalloproteases, and was therefore designated *ADAMTS13*.

B. Characterization of *ADAMTS13* Gene and ADAMTS13 Protein

ADAM (a disintegrin and metalloproteinase) family members are membrane-anchored proteases with diverse functions. Known members include fertilins α and β, implicated in sperm-egg fusion, and the "sheddases" such as TACE (TNFα convertase), which mediate the shedding of cell surface proteins (Blobel,C.P. [1997] Cell *90*, 589-592).. ADAMTS family members are distinguished from ADAMs by the presence of one or more thrombospondin 1-like (TSP1) domain(s) at the C-terminus and by the absence of the EGF repeat, transmembrane domain and cytoplasmic tail typically observed in ADAM metalloproteinases. The TSP1 motifs are thought to mediate interactions with components of the extracellular matrix (Kaushal, G.P. & Shah, S.V. [2000] J. Clin. Invest *105*,1335-1337; Hurskainen, T.L. *et al.* [1999] J. Biol. Chem. *274*, 25555-25563; and Tang, B.L. [2001] Int. J. Biochem. Cell Biol. *33*, 33-44). ADAMTS4 and 5/11 (aggrecanases) cleave the proteoglycan core of articular cartilage and may play a role in inflammatory joint disease (Tortorella, M.D. *et al* [1999] Science *284*, 1664-1666). and mutations in ADAMTS2 (procollagen N-proteinase) result in the connective tissue disorder Ehlers-Danlos Syndrome, Type V (Colige, A. *et al.* [1999] Am. J. Hum. Genet. *65*, 308-317). Though ADAMTS1 mutations have not been identified in humans, genetically deficient mice exhibit growth retardation, adipose tissue abnormalities, and fibrotic changes throughout the genitourinary system, suggesting a critical role for ADAMTS1 in organogenesis and tissue remodeling (Shindo, T. *et al.* [2000] J. Clin. Invest. *105*, 1345-1352). The function and protein substrates for the remaining ADAMTS family members are unknown.

1. ADAMTS13 coding sequence.

The full-length *ADAMTS13* mRNA is 4,550 nucleotides in length, encoding a 1,427 amino acid open reading frame that begins with the first ATG, leaving short 5' and 3' untranslated regions of 61 bp and 208 bp, respectively. The *ADAMTS13* gene spans 29 exons encompassing approximately 37 kb in the human genome and encoding a 1,427 amino acid protein (Figure 3B). Analysis of RT-PCR and cloned cDNA sequences provided evidence for alternative splicing of exon 17, resulting in a frameshift that predicts a truncated 842 amino acid form of the protein lacking the 6 C-terminal TSP1 repeats (as shown in Figures 7 and 8). Comparative analysis with draft mouse genomic sequences demonstrates a high degree of conservation throughout the coding exons and identifies an additional potential exon located between the current exons 22 and 23, which may indicate

another splice isoform. These findings suggest the potential for differentially regulated alternative isoforms of ADAMTS13 with diverse biologic functions in addition to the proteolytic processing of VWF. Alternative splicing has also been observed in other ADAMTS proteins, including ADAMTS9, resulting in a similar variation in the number of C-terminal TSP1 repeats (Tang, B.L. [2001] Int. J. Biochem. Cell Biol. *33*, 33-44).

2. ADAMTS13 protein

The domain structure of ADAMTS13 is depicted at the bottom of Figure 3B. A predicted signal peptide is followed by a short propeptide domain ending in a potential propeptide convertase cleavage site at amino acids 71-74 (RQRR), suggesting that proteolytic processing, either in the trans Golgi or at the cell surface, is required for activation. The protease domain that follows contains a perfect match for the HEXGHXXGXXHD extended catalytic site consensus sequence shared between snake venom metalloproteinases, and ADAM family members (Kaushal, G.P. & Shah, S.V. [2000] J. Clin. Invest *105*: 1335-1337; Blobel, C.P. [1997] Cell *90*, 589-592; and Kuno, K. *et al.* [1997]. J. Biol. Chem. *272*, 556-562). The catalytic domain is followed by the disintegrin, thrombospondin type 1 (TSP1), and spacer domains characteristic of the ADAMTS family. An RGDS sequence not present in other ADAMTSs is located immediately C-terminal to the first TSP1 domain, suggesting a possible novel integrin interaction. The C-terminus contains an additional 6 TSP1 repeats, followed by a segment with homology to a CUB domain. CUB domains have been identified in a number of developmentally regulated proteins (Bork, P. & Beckmann, G. [1993] J. Mol. Biol. *231*, 539-545); however, this domain has not been reported for an ADAMTS protein, and appears to be novel to ADAMTS13. The previously reported inhibitor profile and metal cation dependence of the VWF-cleaving protease (Tsai, H.M. [1996] Blood *87*, 4235-4244; Furlan, *et al.* [1996] Blood *87*, 4223-4234; Tsai, *et al.* [1997] Blood *89*, 1954-1962) are consistent with its identity as an ADAMTS. The predicted, nonglycosylated molecular mass of ADAMTS13 is 154 kd, consistent with a previously estimated mass of 200 kd for partially purified VWF-cleaving protease (Tsai, H.M. [1996] Blood *87*, 4235-4244), though considerably smaller than the 300 kd mass reported by other (Furlan *et al.* [1996] Blood *87*, 4223-4234).

3. ADAMTS13 expression and activity

The full-length *ADAMTS13* cDNA was assembled and cloned into a mammalian expression vector and transfected into CHO-Tag cells (as described in the Examples). Conditioned medium from transfected cells was tested for VWF-cleaving protease activity by a previously-described assay (Tsai *et al.* [2001] Clin. Lab *47*, 387-392) and was found to exhibit a VWF-cleaving protease activity of 0.47 U (+/- 0.07), as compared to a value of 0.06 (+/- 0.03) in conditioned media from mock-transfected cells ($p<0.01$). These data directly demonstrate the VWF-cleaving protease activity of recombinant ADAMTS13.

These results demonstrate the feasibility of producing recombinant ADAMTS13 and confirm that the latter possesses VWF-cleaving protease activity. The VWF-cleaving protease assay used here (Tsai *et al.* [2001] Clin. Lab *47*, 387-392) relies on the detection of the 176 kD dimer formed by VWF cleavage at the peptide bond between Tyr842 and Met843 (Dent *et al.* [1990] Proc. Natl. Acad. Sci. U.S.A. *87*, 6306-6310), further indicating that cleavage of VWF by recombinant ADAMTS13 occurs at or near this bond. These results support the use of providing an active form ADAMTS13 for the treatment of TTP; moreover, it is contemplated that the production of recombinant protein will facilitate the development of improved diagnostic reagents for both familial and acquired forms of TTP.

C. Mutants and variants of *ADAMTS13*

1. Mutants of *ADAMTS13* Cause Familial TTP.

DNA sequence analysis identified mutations within the *ADAMTS13* gene in all 4 of the pedigrees depicted in Figure 1, as well as in 3 additional TTP patients not included in the original genome scan (families E-G, Table 1). These mutations are shown in Table 1.

Table 1:

ADAMTS13 mutations in Thrombotic Thrombocytopenic Purpura (TTP).

Genomic DNA from patients was used to amplify exons and intron/exon boundaries of *ADAMTS13*. For mutations in families A to D, candidate mutations were confirmed in both parents. Analysis of the potential splice mutation in family G with a splice site prediction tool (http://www.fruitfly.org/seq_tools/splice.html) suggests that it should abolish splicing from this donor site. Consistent with this prediction, sequence analysis of PCR amplified mRNA from patient lymphoblasts identified a major product of wild-type sequence derived only from the normal allele. A second, slightly larger product not seen in control samples

was derived only from the mutant allele, utilizing a cryptic donor splice site at +69, resulting in a 23 amino acid insertion. Approximately 180 normal control chromosomes were screened by allele-specific oligonucleotide hybridization, restriction digest or PCR for the following mutations, with no mutant alleles identified: H96D, R102C, R398H, R528G, R692C, C1213Y, 2374-2399del, and 1584+5G>A.

exon	family	nucleotide	amino acid
3	B	286C>G	H96D
3	E	304C>T	R102C
6	E	587C>T	T196I
10	D	1193G>A	R398H
13	C	1582A>G	R528G
13	G	1584+5G>A	splice
17	A	2074C>T	R692C
19	F	2374-2399del	frameshift
22	B	2851T>G	C951G
24	D	3070T>G	C1024G
26	F	3638G>A	C1213Y
26 *	8 *	3655C>T *	R1219W *
27	C	3769-3770insA	frameshift

An additional mutation accounting for 1 of 2 disease alleles in an 8th familial pedigree was also identified (indicated in Table 1 above by an asterisk (*)). Sequence analysis of exons and exon-intron junctions of *ADAMTS13* was performed on genomic DNA obtained from the proband of an additional familial TTP pedigree. The patient was found to be heterozygous for a 3655C>T substitution in exon 26. The substitution was also present in the heterozygous state in the affected brother and obligate carrier father, but absent in the mother and 6 unaffected siblings. In addition, the T allele was confirmed to be absent from 180 control chromosomes by allele-specific oligonucleotide hybridization. The resulting amino acid change, R1219W, occurs within the CUB domain at the C-terminus of ADAMTS13 (Figure 3, panel C). No mutation was identified for the other allele in this family.

The 12 mutations initially identified accounted for all but one of the 15 disease alleles initially expected in this set of patients (Table 1). With the additional mutation (which accounts for 1 of 2 disease alleles in the 8th family pedigree), these analyses resulted in the identification of 15 of the 17 disease alleles in the families studied. The two unidentified mutations may lie within exon 7, or within noncoding regions not covered by the sequence analysis. The presence of at least one mutation in all hereditary TTP families identified thus far indicates that most if not all cases of this disease are due to mutations in *ADAMTS13*. Moreover, successful identification of 15 of 17 disease alleles suggests that the majority of *ADAMTS13* mutations in hereditary TTP are likely to lie within the coding sequence and exert effects on either protein stability or function.

No recurrent mutation was observed, except in family A, where all 3 affected individuals are homozygous for the same mutation carried on the same extended haplotype, suggesting a founder mutation within the South American population of origin for this family. Two mutations result in frameshifts (a 26 bp deletion in exon 19 and single A insertion in exon 27) and a single splice mutation leads to an in frame 23 amino acid insertion. The remaining observed mutations all result in nonconservative amino acid substitutions (Table 1 and following paragraph), and all occur at positions that are perfectly conserved between the human and murine genes; these mutations are also located throughout the length of the protein, with no apparent clustering in any specific domain or region of the molecule.

However, several of these mutations occur at highly conserved positions that could disrupt proper folding or may affect substrate binding. The R398H mutation within the first TSP1 motif occurs at a residue that is perfectly conserved among all 18 ADAMTS family

members identified to date. This mutation occurs within a conserved motif of the TSP1 domains shown to be modified by an unusual O-linked disaccharide Glc-Fuc-O-Ser/Thr in platelet TSP1 (Hofsteenge *et al.* [2001] J. Biol. Chem. *276*, 6485-6498) and thought to be important for ligand binding (Adams & Tucker [2000] Dev. Dyn. *218*, 280-299). H96D in the metalloprotease domain occurs at a residue that is also conserved in all ADAMTS family members identified to date, with the exception of ADAMTS5/11 and ADAMTS8. The R102C mutation introduces a cysteine residue which may disrupt a disulfide bond between C155 and C208, predicted based on a comparison with a molecular model of adamalysin II (Zheng *et al.* [2001] J. Biol. Chem. *276*, 41059-41063). The C951G mutation (as well as the C1024G mutation) also affect conserved cysteine residues (Adams & Tucker [2000] Dev. Dyn. *218*, 280-299; Zheng *et al.* [2001] J. Biol. Chem. *276*, 41059-41063) in the fourth and sixth TSP1 motifs of ADAMTS13, respectively. The C1213Y and R1219W mutations occur within the CUB domain located at the C-terminus of ADAMTS13. The C1213Y mutation affects one of several highly conserved cysteine residues within CUB domains (http://pfam.wustl.edu) that have been proposed to form disulfide bonds (Sieron *et al.* [2000] Biochemistry *39*, 3231-3239). CUB domains have been described in a number of developmentally regulated proteins, including several zinc metalloproteases (Bork & Beckmann [1993] J. Mol. Biol. *231*, 539-545); the CUB domain of BMP-1, or procollagen-C-proteinase, has been implicated in substrate binding (Sieron *et al.* [2000] Biochemistry *39*, 3231-3239).

The spectrum of *ADAMTS13* mutations observed here is notable for the relative paucity of obvious null alleles. In addition, both frameshift mutations are located toward the C-terminus, potentially giving rise to truncated forms of the protease that retain an intact catalytic domain. These data suggest that complete deficiency of ADAMTS13 may be lethal. This hypothesis is supported by the observed trend toward trace activity above background seen in the majority of the mutants tested, and by the low levels of residual VWF-cleaving protease activity observed in all 10 deficient patients described here (0.02 to 0.07 U/ml).

Northern blot analysis detected an ~4.7 kb *ADAMTS13* mRNA specifically in the liver, with a truncated, ~2.3 kb, mRNA faintly visible in placenta (Figure 4A). These data suggest that plasma VWF-cleaving protease may be derived primarily from *ADAMTS13* expression in the liver. The strong RT-PCR signal seen in the ovary, and variable expression in other tissues (Figure 4B), suggest other potential functions for this protein. The absence of detectable transcripts in other highly vascular tissues such as the lung,

kidney and heart may indicate that the vascular endothelium is not a primary site of *ADAMTS13* expression.

The findings reported here provide the first direct proof of an etiologic role for a VWF-cleaving protease in the pathogenesis of TTP and identify the enzyme associated with this activity as the novel metalloproteinase ADAMTS13. These data are consistent with the hypothesis that accumulation of hyperactive large VWF multimers in the absence of normal proteolytic processing triggers pathologic platelet aggregation and is the direct mechanism responsible for TTP. Alternatively, decreased VWF proteolysis may be a marker for the loss of ADAMTS13 activity. ADAMTS13 may also have important biologic functions elsewhere in the coagulation system or in the blood vessel wall, with loss of one or more of these activities providing the direct link to the pathogenesis of TTP.

2. *ADAMTS13* mutations in TTP patients result in loss of VWF-cleaving protease activity.

The functional significance of the *ADAMTS13* mutations identified here was evaluated by analysis of the VWF-cleaving protease activity of recombinant mutant *ADAMTS13*. Each of the missense mutations was engineered into the wild-type *ADAMTS13* construct and transfected into CHO-Tag cells. Analysis of VWF-cleaving protease activity in conditioned media revealed that all 9 mutations examined resulted in markedly decreased activity, which is not statistically distinguishable from that present in conditioned media from mock-transfected cells (Figure 11).

Conditioned media from CHO-Tag cells transfected with the wild-type and the missense mutant constructs were subjected to Western blot analysis with 4 different anti-peptide antibodies raised against ADAMTS13 peptides. Although one of these antibodies (antibody 4, see Materials and Methods in the Examples) has been successfully used to detect appropriate segments of bacterially-expressed ADAMTS13, no specific fragments corresponding to the expected size of ADAMTS13 were detectable in conditioned media from cells transfected with either the wild-type or mutant constructs. In addition, epitope (FLAG)-tagged recombinant ADAMTS13 was also undetectable by Western blot analysis using a commercially-available anti-FLAG antibody.

Though all 9 mutations described above exhibit marked loss of VWF-cleaving protease activity, the loss of activity may be due to change in protein function, synthesis, secretion, or stability. The plasma concentration of ADAMTS13 has been estimated at ~1 mg/ml (Gerritsen *et al.* [2001] Blood *98*, 1654-1661). Therefore, based on the VWF-

cleaving protease activity of wild-type recombinant ADAMTS13, mutant ADAMTS13 is present at roughly half this concentration in the recombinant mutant ADAMTS13 samples. Although initial attempts to determine whether mutant proteins are secreted from the cell at levels similar to wild-type recombinant ADAMTS13 by Western blot analysis were unsuccessful, as described above, it is contemplated that generation of more sensitive antibody reagents or of epitope-tagged mutant constructs will result in such determination.

3. Variants of *ADAMTS13*.

A large number of SNPs were also identified, though only 7/25 result in amino acid substitutions (see Table 2). These SNPs all constitute naturally occurring wild-type *ADAMTS13* alleles; any particular allele may comprise from one to more than one SNP, and different combinations of SNPs may occur together.

Table 2:

Single nucleotide polymorphisms

exon/ intron	nucleotide	amino acid
ex1	19C>T	R7W
ex4	354G>A	silent
ex5	420T>C	silent
ex6	582C>T	silent
int6	686+4T>G	N/A
int8	987+11C>T	N/A
int8	987+69C>T	N/A
int9	1092+67G>A	N/A
int10	1245-32C>G	N/A
ex12	1342C>G	Q448E
int13	1584+106C>G	N/A
int13	1584+236T>C	N/A
ex15	1716G>A	silent
int15	1787-26G>A	N/A
ex16	1852C>G	P618A
ex16	1874G>A	R625H

ex18	2195C>T	A732V
ex19	2280T>C	silent
ex21	2699C>T	A900V
int22	2861+55C>T	N/A
ex23	2910C>T	silent
ex24	3097G>A	A1033T
ex24	3108G>A	silent
int28	4077+32T>C	N/A
ex29	4221C>A	silent

Of the 25 single nucleotide polymorphisms (SNPs) identified in *ADAMTS13* genomic sequences, 15 polymorphisms occurred within coding sequence, and 7 cause amino acid substitutions. This surprising degree of polymorphism in the *ADAMTS13* gene raises the possibility that one or more of the putative disease mutation identified in the initial panel of patients, though absent from 180 control chromosomes, might represent a rare "private" polymorphism within the corresponding family. However, the functional data shown in Figure 11 demonstrate that all 9 mutations described above represent authentic disease mutations resulting in partial or complete loss of ADAMTS13 function.

D. Utility of *ADAMTS13* Genes and Proteins

The present invention also provides several methods of use of wild-type and mutants, variants and fragments of *ADAMTS13* and the encoded proteins, as well as of antibodies to wild-type and mutants, variants, and fragments of ADAMTS13. In some embodiments, methods are provided for precise and rapid diagnosis of TTP in individuals with inherited TTP. Such diagnosis is effected by any number of detection assays based upon nucleotide sequences, as described in more detail below, in which the types of alleles present in an individual are identified. In other embodiments, rapid diagnosis of TTP both in the inherited and in the more common acquired form of TTP is based upon the use of antibodies to detect the presence or levels of ADAMTS13 and variants and mutants, as for example in blood or plasma samples obtained from in individual.

The identification of ADAMTS13 deficiency as the cause of TTP also has major implications for the treatment of this important human disease. In these embodiments, the present invention provides methods of treating patients with TTP. In some embodiments, a

patient is administered a therapeutically effective amount of a recombinant protein. This treatment is likely to be much more effective, as well as much safer, than the plasma replacement therapy that is currently the only alternative. In yet other embodiments, a patient is treated with a therapeutically effective amount of genetic material comprising an *ADAMTS13* gene or mutant or variant thereof that results in production of an ADAMTS13 protease in the patient.

In addition, ADAMTS13 or variants or other drugs based upon this protease can also be used in several different ways. In some embodiments, ADAMTS13 or drugs developed from it can be used in normal individuals as a novel approach to effect anticoagulation (preventing abnormal blood clots). Since blood clots are the basis of many important human diseases including heart attack and stroke, ADAMTS13 is used itself or as a suitable platform for the development of new pharmaceuticals to treat these common human diseases, where the pharmaceuticals are anticoagulants. In other embodiments, ADAMTS13 or variants are used to deliver other therapeutic proteins specifically to the microvasculature. These embodiments are based upon the observation that ADAMTS13 uses VWF in a specific conformation to cleave the Met842-Tyr843 bond. This conformation is reproduced *in vitro* by slightly "denaturing" VWF in urea or guanidine. It is believed that such "denaturation" is achieved *in vivo* by shear stress in the microvasculature. Therefore, it is contemplated that therapeutic proteins are administered in an inactive form that can be activated by cleavage of a peptide bond specifically by ADAMTS13 or variants under conditions of high shear stress *in vivo*.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to a disintegrin and metalloproteinase containing thrombospondin 1-like domains (ADAMTS) and in particular to a novel ADAMTS13 protease and to nucleic acids encoding ADAMTS13 proteases. The present invention encompasses both native and recombinant wild-type forms of ADAMTS13, as well as mutant and variant forms including fragments, some of which posses altered characteristics relative to the wild-type ADAMTS13. The present invention also relates to methods of using ADAMTS13, including for treatment of TTP. The present invention also relates to methods for screening for the presence of TTP. The present invention further relates to methods for developing anticoagulant drugs based upon ADAMTS13.

I. *ADAMTS13* Polynucleotides

As described above, a novel member of the family of disintegrin and metalloproteinases containing thrombospondin 1-like domains, ADAMTS13, has been discovered. This was accomplished by studying a series of families in which TTP appears to be inherited and then using a positional cloning approach to map a gene responsible for reduced VWF-cleaving protease activity to a locus on 9q34. Accordingly, the present invention provides nucleic acids encoding *ADAMTS13* genes, homologs, variants (*e.g.*, polymorphisms and mutants), and fragments, including but not limited to, those described in SEQ ID NOs: 1, 3, 5 and 7. In some embodiments, the present invention provide polynucleotide sequences that are capable of hybridizing to SEQ ID NOs: 1, 3, 5, and 7 under conditions of low to high stringency as long as the polynucleotide sequence capable of hybridizing encodes a protein that retains at least one or a portion of at least one biological activity of a naturally occurring ADAMTS13. In some embodiments, the protein that retains at least one or a portion of at least one biological activity of naturally occurring ADAMTS13 is 70% homologous to wild-type ADAMTS13, preferably 80% homologous to wild-type ADAMTS13, more preferably 90% homologous to wild-type ADAMTS13, and most preferably 95% homologous to wild-type ADAMTS13. In preferred embodiments, hybridization conditions are based on the melting temperature (T_m) of the nucleic acid binding complex and confer a defined "stringency" as explained above (*See e.g.*, Wahl, *et al.*, [1987] Meth. Enzymol., 152:399-407, incorporated herein by reference).

In other embodiments of the present invention, additional alleles of *ADAMTS13* are provided. In preferred embodiments, alleles result from a polymorphism or mutation (*i.e.*, a change in the nucleic acid sequence) and generally produce altered mRNAs or polypeptides whose structure or function may or may not be altered. Any given gene may have none, one or many allelic forms. Common mutational changes that give rise to alleles are generally ascribed to deletions, additions or substitutions of nucleic acids. Each of these types of changes may occur alone, or in combination with the others, and at the rate of one or more times in a given sequence. Non-limiting examples of the alleles of the present invention include those encoded by SEQ ID NOs:1, 3, 5, and 7 (wild type), as well as those described in Tables 1 and 2.

In some embodiments of the present invention, the nucleotide sequences encode a CUB domain (*e.g.*, nucleic acid sequences encoding the polypeptide fragment from amino acid 1192 to amino acid 1286 as shown in Figure 6).

In still other embodiments of the present invention, the nucleotide sequences of the present invention may be engineered in order to alter an ADAMTS13 coding sequence for a variety of reasons, including but not limited to, alterations which modify the cloning, processing and/or expression of the gene product. For example, mutations may be introduced using techniques that are well known in the art (*e.g.*, site-directed mutagenesis to insert new restriction sites, to alter glycosylation patterns, to change codon preference, etc.).

In some embodiments of the present invention, the polynucleotide sequence of *ADAMTS13* may be extended utilizing the nucleotide sequences (*e.g.*, SEQ ID NOs: 1, 3 and 7) in various methods known in the art to detect upstream sequences such as promoters and regulatory elements. For example, it is contemplated that restriction-site polymerase chain reaction (PCR) will find use in the present invention. This is a direct method which uses universal primers to retrieve unknown sequence adjacent to a known locus (Gobinda *et al.* [1993] PCR Methods Applic., 2:318-22). First, genomic DNA is amplified in the presence of a primer to a linker sequence and a primer specific to the known region. The amplified sequences are then subjected to a second round of PCR with the same linker primer and another specific primer internal to the first one. Products of each round of PCR are transcribed with an appropriate RNA polymerase and sequenced using reverse transcriptase.

In another embodiment, inverse PCR can be used to amplify or extend sequences using divergent primers based on a known region (Triglia *et al.* [1988] Nucleic Acids Res., 16:8186). The primers may be designed using Oligo 4.0 (National Biosciences Inc, Plymouth Minn.), or another appropriate program, to be 22-30 nucleotides in length, to have a GC content of 50% or more, and to anneal to the target sequence at temperatures about 68-72°C. The method uses several restriction enzymes to generate a suitable fragment in the known region of a gene. The fragment is then circularized by intramolecular ligation and used as a PCR template. In still other embodiments, walking PCR is utilized. Walking PCR is a method for targeted gene walking that permits retrieval of unknown sequence (Parker *et al.*, [1991] Nucleic Acids Res., 19:3055-3060). The PROMOTERFINDER kit (Clontech) uses PCR, nested primers and special libraries to "walk in" genomic DNA. This process avoids the need to screen libraries and is useful in finding intron/exon junctions.

Preferred libraries for screening for full length cDNAs include mammalian libraries that have been size-selected to include larger cDNAs. Also, random primed libraries are preferred, in that they will contain more sequences that contain the 5' and upstream gene regions. A randomly primed library may be particularly useful in case where an oligo d(T)

library does not yield full-length cDNA. Genomic mammalian libraries are useful for obtaining introns and extending 5' sequence.

In other embodiments of the present invention, variants of the disclosed *ADAMTS13* sequences are provided. In preferred embodiments, variants result from polymorphisms or mutations (*i.e.*, a change in the nucleic acid sequence) and generally produce altered mRNAs or polypeptides whose structure or function may or may not be altered. Any given gene may have none, one, or many variant forms. Non-limiting examples of variants are shown in Table 2 Common mutational changes that give rise to variants are generally ascribed to deletions, additions or substitutions of nucleic acids; non-limiting examples are shown in Table 1. Each of these types of changes may occur alone, or in combination with the others, and at the rate of one or more times in a given sequence.

It is contemplated that it is possible to modify the structure of a peptide having a function (*e.g.*, ADAMTS13 protease function) for such purposes as altering (*e.g.*, increasing or decreasing) the substrate specificity or selectivity affinity of the ADAMTS13 for VWF or another substrate. Such modified peptides are considered functional equivalents of peptides having an activity of ADAMTS13 as defined herein. A modified peptide can be produced in which the nucleotide sequence encoding the polypeptide has been altered, such as by substitution, deletion, or addition. In particularly preferred embodiments, these modifications do not significantly reduce the protease activity of the modified ADAMTS13. In other words, construct "X" can be evaluated in order to determine whether it is a member of the genus of modified or variant ADAMTS13's of the present invention as defined functionally, rather than structurally. In preferred embodiments, the activity of variant ADAMTS13 polypeptides is evaluated by the methods described in Example 1B. Accordingly, in some embodiments, the present invention provides nucleic acids encoding a ADAMTS13 that cleaves VWF. In preferred embodiments, the activity of a ADAMTS13 variant is evaluated by utilizing guanidine hydrochloride-treated VWF.

Moreover, as described above, variant forms of ADAMTS13 and nucleotides encoding the same are also contemplated as being equivalent to those peptides and DNA molecules that are set forth in more detail herein. For example, it is contemplated that isolated replacement of a leucine with an isoleucine or valine, an aspartate with a glutamate, a threonine with a serine, or a similar replacement of an amino acid with a structurally related amino acid (*i.e.*, conservative mutations) will not have a major effect on the biological activity of the resulting molecule. Accordingly, some embodiments of the present invention provide variants of ADAMTS13 disclosed herein containing conservative

replacements. Conservative replacements are those that take place within a family of amino acids that are related in their side chains. Genetically encoded amino acids can be divided into four families: (1) acidic (aspartate, glutamate); (2) basic (lysine, arginine, histidine); (3) nonpolar (alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan); and (4) uncharged polar (glycine, asparagine, glutamine, cysteine, serine, threonine, tyrosine). Phenylalanine, tryptophan, and tyrosine are sometimes classified jointly as aromatic amino acids. In similar fashion, the amino acid repertoire can be grouped as (1) acidic (aspartate, glutamate); (2) basic (lysine, arginine, histidine), (3) aliphatic (glycine, alanine, valine, leucine, isoleucine, serine, threonine), with serine and threonine optionally be grouped separately as aliphatic-hydroxyl; (4) aromatic (phenylalanine, tyrosine, tryptophan); (5) amide (asparagine, glutamine); and (6) sulfur -containing (cysteine and methionine) (*e.g.*, Stryer ed., *Biochemistry*, pg. 17-21, 2nd ed, WH Freeman and Co., 1981). Whether a change in the amino acid sequence of a peptide results in a functional polypeptide can be readily determined by assessing the ability of the variant peptide to function in a fashion similar to the wild-type protein. Peptides having more than one replacement can readily be tested in the same manner.

More rarely, a variant includes "nonconservative" changes (*e.g.*, replacement of a glycine with a tryptophan). Analogous minor variations can also include amino acid deletions or insertions, or both. Guidance in determining which amino acid residues can be substituted, inserted, or deleted without abolishing biological activity can be found using computer programs (*e.g.*, LASERGENE software, DNASTAR Inc., Madison, Wis.).

As described in more detail below, variants may be produced by methods such as directed evolution or other techniques for producing combinatorial libraries of variants, described in more detail below. In still other embodiments of the present invention, the nucleotide sequences of the present invention may be engineered in order to alter a ADAMTS13 coding sequence including, but not limited to, alterations that modify the cloning, processing, localization, secretion, and/or expression of the gene product. Such mutations may be introduced using techniques that are well known in the art (*e.g.*, site-directed mutagenesis to insert new restriction sites, alter glycosylation patterns, or change codon preference, etc.).

II. ADAMTS13 Polypeptides

In other embodiments, the present invention provides ADAMTS13 polypeptides and fragments. Non-limiting examples of ADAMTS13 polypeptides (*e.g.*, SEQ ID NOs: 2, 4 and 6) are described in Figures 3, 6, and 7. Other embodiments of the present invention provide fusion proteins or functional equivalents of these ADAMTS13 proteins. In still other embodiments, the present invention provides ADAMTS13 polypeptide variants, homologs, and mutants. In some embodiments of the present invention, the polypeptide is a naturally purified product, in other embodiments it is a product of chemical synthetic procedures, and in still other embodiments it is produced by recombinant techniques using a prokaryotic or eukaryotic host (*e.g.*, by bacterial, yeast, higher plant, insect and mammalian cells in culture). In some embodiments, depending upon the host employed in a recombinant production procedure, the polypeptide of the present invention may be glycosylated or it may be non-glycosylated. In other embodiments, the polypeptides of the invention may also include an initial methionine amino acid residue.

In one embodiment of the present invention, due to the inherent degeneracy of the genetic code, DNA sequences other than the polynucleotide sequences of SEQ ID NO:1 and 3 which encode substantially the same or a functionally equivalent amino acid sequences, may be used to clone and express ADAMTS13. In general, such polynucleotide sequences hybridize to SEQ ID NO:1 under conditions of high to medium stringency as described above. As will be understood by those of skill in the art, it may be advantageous to produce ADAMTS13-encoding nucleotide sequences possessing non-naturally occurring codons. Therefore, in some preferred embodiments, codons preferred by a particular prokaryotic or eukaryotic host (Murray *et al.* [1989] Nucl. Acids Res. 17) are selected, for example, to increase the rate of ADAMTS13 expression or to produce recombinant RNA transcripts having desirable properties, such as a longer half-life, than transcripts produced from naturally occurring sequence.

A. Vectors for Production of ADAMTS13

The polynucleotides of the present invention may be employed for producing polypeptides by recombinant techniques. Thus, for example, the polynucleotide may be included in any one of a variety of expression vectors for expressing a polypeptide. In some embodiments of the present invention, vectors include, but are not limited to, chromosomal, nonchromosomal and synthetic DNA sequences (*e.g.*, derivatives of SV40, bacterial plasmids, phage DNA; baculovirus, yeast plasmids, vectors derived from combinations of plasmids and phage DNA, and viral DNA such as vaccinia, adenovirus, fowl pox virus, and

pseudorabies). It is contemplated that any vector may be used as long as it is replicable and viable in the host.

In particular, some embodiments of the present invention provide recombinant constructs comprising one or more of the sequences as broadly described above (*e.g.*, SEQ ID NOS: 1, 3, and 5). In some embodiments of the present invention, the constructs comprise a vector, such as a plasmid or viral vector, into which a sequence of the invention has been inserted, in a forward or reverse orientation. In still other embodiments, the heterologous structural sequence (*e.g.*, SEQ ID NO:1) is assembled in appropriate phase with translation initiation and termination sequences. In preferred embodiments of the present invention, the appropriate DNA sequence is inserted into the vector using any of a variety of procedures. In general, the DNA sequence is inserted into an appropriate restriction endonuclease site(s) by procedures known in the art.

Large numbers of suitable vectors are known to those of skill in the art, and are commercially available. Such vectors include, but are not limited to, the following vectors: 1) Bacterial -- pQE70, pQE60, pQE-9 (Qiagen), pBS, pD10, phagescript, psiX174, pbluescript SK, pBSKS, pNH8A, pNH16a, pNH18A, pNH46A (Stratagene); ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia); 2) Eukaryotic -- pWLNEO, pSV2CAT, pOG44, PXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia); and 3) Baculovirus – pPbac and pMbac (Stratagene). Any other plasmid or vector may be used as long as they are replicable and viable in the host. In some preferred embodiments of the present invention, mammalian expression vectors comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation sites, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking non-transcribed sequences. In other embodiments, DNA sequences derived from the SV40 splice, and polyadenylation sites may be used to provide the required non-transcribed genetic elements.

In certain embodiments of the present invention, the DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. Promoters useful in the present invention include, but are not limited to, the LTR or SV40 promoter, the *E. coli lac* or *trp*, the phage lambda P_L and P_R, T3 and T7 promoters, and the cytomegalovirus (CMV) immediate early, herpes simplex virus (HSV) thymidine kinase, and mouse metallothionein-I promoters and other promoters known to control expression of gene in prokaryotic or eukaryotic cells or their viruses. In other embodiments of the present invention, recombinant expression vectors

include origins of replication and selectable markers permitting transformation of the host cell (*e.g.*, dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or tetracycline or ampicillin resistance in *E. coli*).

In some embodiments of the present invention, transcription of the DNA encoding the polypeptides of the present invention by higher eukaryotes is increased by inserting an enhancer sequence into the vector. Enhancers are *cis*-acting elements of DNA, usually about from 10 to 300 bp that act on a promoter to increase its transcription. Enhancers useful in the present invention include, but are not limited to, the SV40 enhancer on the late side of the replication origin bp 100 to 270, a cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

In other embodiments, the expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. In still other embodiments of the present invention, the vector may also include appropriate sequences for amplifying expression.

B. Host Cells for Production of ADAMTS13

In a further embodiment, the present invention provides host cells containing the above-described constructs. In some embodiments of the present invention, the host cell is a higher eukaryotic cell (*e.g.*, a mammalian or insect cell). In other embodiments of the present invention, the host cell is a lower eukaryotic cell (*e.g.*, a yeast cell). In still other embodiments of the present invention, the host cell can be a prokaryotic cell (*e.g.*, a bacterial cell). Specific examples of host cells include, but are not limited to, *Escherichia coli*, *Salmonella typhimurium*, *Bacillus subtilis*, and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, as well as *Saccharomycees cerivisiae*, *Schizosaccharomycees pombe*, *Drosophila* S2 cells, *Spodoptera* Sf9 cells, Chinese hamster ovary (CHO) cells, COS-7 lines of monkey kidney fibroblasts, (Gluzman, Cell 23:175 [1981]), C127, 3T3, 293, 293T, HeLa and BHK cell lines, T-1 (tobacco cell culture line), root cell and cultured roots in rhizosecretion (Gleba *et al.*, [1999] Proc Natl Acad Sci USA 96:5973-5977).

The constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. In some embodiments, introduction of the construct into the host cell can be accomplished by calcium phosphate transfection, DEAE-Dextran mediated transfection, or electroporation (*See e.g.*, Davis *et al.* [1986] Basic Methods in Molecular Biology). Alternatively, in some embodiments of the present

invention, the polypeptides of the invention can be synthetically produced by conventional peptide synthesizers.

Proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, *et al.* (1989) Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor, N.Y.

In some embodiments of the present invention, following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period. In other embodiments of the present invention, cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification. In still other embodiments of the present invention, microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

C. Purification of ADAMTS13

The present invention also provides methods for recovering and purifying ADAMTS13 from recombinant cell cultures including, but not limited to, ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. In other embodiments of the present invention, protein-refolding steps can be used as necessary, in completing configuration of the mature protein. In still other embodiments of the present invention, high performance liquid chromatography (HPLC) can be employed for final purification steps.

The present invention further provides polynucleotides having the coding sequence (*e.g.*, SEQ ID NOs: 1, 3, and 5) fused in frame to a marker sequence that allows for purification of the polypeptide of the present invention. A non-limiting example of a marker sequence is a hexahistidine tag which may be supplied by a vector, preferably a pQE-9 vector, which provides for purification of the polypeptide fused to the marker in the case of a bacterial host, or, for example, the marker sequence may be a hemagglutinin (HA)

tag when a mammalian host (*e.g.*, COS-7 cells) is used. The HA tag corresponds to an epitope derived from the influenza hemagglutinin protein (Wilson *et al.* [1984] Cell, 37:767).

D. Fragments and Domains of ADAMTS13

In addition, the present invention provides fragments of ADAMTS13 (*i.e.*, truncation mutants, *e.g.*, SEQ ID NO:4). In other embodiments, the present invention provides domains of ADAMTS13 (*e.g.*, the CUB domain, SEQ ID NO:6) In some embodiments of the present invention, when expression of a portion of the ADAMTS13 protein is desired, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from *E. coli* (Ben-Bassat *et al.* [1987] J. Bacteriol., 169:751) and *Salmonella typhimurium* and its *in vitro* activity has been demonstrated on recombinant proteins (Miller *et al.* [1990] Proc. Natl. Acad. Sci. USA, 84:2718). Therefore, removal of an N-terminal methionine, if desired, can be achieved either *in vivo* by expressing such recombinant polypeptides in a host which produces MAP (*e.g.*, *E. coli* or CM89 or *S. cerevisiae*), or *in vitro* by use of purified MAP.

E. Fusion Proteins Containing ADAMTS13

The present invention also provides fusion proteins incorporating all or part of ADAMTS13. Accordingly, in some embodiments of the present invention, the coding sequences for the polypeptide can be incorporated as a part of a fusion gene including a nucleotide sequence encoding a different polypeptide. It is contemplated that this type of expression system will find use under conditions where it is desirable to produce an immunogenic fragment of a ADAMTS13 protein. In some embodiments of the present invention, the VP6 capsid protein of rotavirus is used as an immunologic carrier protein for portions of the ADAMTS13 polypeptide, either in the monomeric form or in the form of a viral particle. In other embodiments of the present invention, the nucleic acid sequences corresponding to the portion of ADAMTS13 against which antibodies are to be raised can be incorporated into a fusion gene construct which includes coding sequences for a late vaccinia virus structural protein to produce a set of recombinant viruses expressing fusion proteins comprising a portion of ADAMTS13 as part of the virion. It has been demonstrated with the use of immunogenic fusion proteins utilizing the hepatitis B surface

antigen fusion proteins that recombinant hepatitis B virions can be utilized in this role as well. Similarly, in other embodiments of the present invention, chimeric constructs coding for fusion proteins containing a portion of ADAMTS13 and the poliovirus capsid protein are created to enhance immunogenicity of the set of polypeptide antigens (*See e.g.*, EP Publication No. 025949; and Evans *et al.* (1989) Nature 339:385; Huang *et al.* (1988) J. Virol., 62:3855; and Schlienger *et al.* (1992) J. Virol., 66:2).

In still other embodiments of the present invention, the multiple antigen peptide system for peptide-based immunization can be utilized. In this system, a desired portion of ADAMTS13 is obtained directly from organo-chemical synthesis of the peptide onto an oligomeric branching lysine core (*see e.g.*, Posnett *et al.* (1988) J. Biol. Chem., 263:1719; and Nardelli *et al.* (1992) J. Immunol., 148:914). In other embodiments of the present invention, antigenic determinants of the ADAMTS13 proteins can also be expressed and presented by bacterial cells.

In addition to utilizing fusion proteins to enhance immunogenicity, it is widely appreciated that fusion proteins can also facilitate the expression of proteins, such as the ADAMTS13 protein of the present invention. Accordingly, in some embodiments of the present invention, ADAMTS13 can be generated as a glutathione-S-transferase (*i.e.*, GST fusion protein). It is contemplated that such GST fusion proteins will enable easy purification of ADAMTS13, such as by the use of glutathione-derivatized matrices (*See e.g.*, Ausabel *et al.* (1992) (eds.), Current Protocols in Molecular Biology, John Wiley & Sons, NY). In another embodiment of the present invention, a fusion gene coding for a purification leader sequence, such as a poly-(His)/enterokinase cleavage site sequence at the N-terminus of the desired portion of ADAMTS13, can allow purification of the expressed ADAMTS13 fusion protein by affinity chromatography using a Ni^{2+} metal resin. In still another embodiment of the present invention, the purification leader sequence can then be subsequently removed by treatment with enterokinase (*See e.g.*, Hochuli *et al.* (1987) J. Chromatogr., 411:177; and Janknecht *et al.*, Proc. Natl. Acad. Sci. USA 88:8972).

Techniques for making fusion genes are well known. Essentially, the joining of various DNA fragments coding for different polypeptide sequences is performed in accordance with conventional techniques, employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment of the present invention, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers.

Alternatively, in other embodiments of the present invention, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed to generate a chimeric gene sequence (*See e.g.*, Current Protocols in Molecular Biology, *supra*).

F. **Variants of ADAMTS13**

Still other embodiments of the present invention provide mutant or variant forms of ADMTS13 (*i.e.*, muteins; see for example Table 1). It is possible to modify the structure of a peptide having an activity of ADAMTS13 for such purposes as enhancing therapeutic or prophylactic efficacy, or stability (*e.g.*, *ex vivo* shelf life, and/or resistance to proteolytic degradation *in vivo*). Such modified peptides are considered functional equivalents of peptides having an activity of the subject ADAMTS13 proteins as defined herein. A modified peptide can be produced in which the amino acid sequence has been altered, such as by amino acid substitution, deletion, or addition.

Moreover, as described above, variant forms (*e.g.*, mutants or polymorphic sequences) of the subject ADAMTS13 proteins and the nucleotides encoding them are also contemplated as being equivalent to those peptides and DNA molecules that are set forth in more detail. For example, as described above, the present invention encompasses mutant and variant proteins that contain conservative or non-conservative amino acid substitutions.

This invention further contemplates a method of generating sets of combinatorial mutants of the present ADAMTS13 proteins, as well as truncation mutants, and is especially useful for identifying potential variant sequences (*i.e.*, mutants or polymorphic sequences) that are functional in cleaving VWF proteins or other protein substrates. The purpose of screening such combinatorial libraries is to generate, for example, novel ADAMTS13 variants that can act as anticoagulants.

Therefore, in some embodiments of the present invention, ADAMTS13 variants are engineered by the present method to provide altered substrate specificity or selectivity. In other embodiments of the present invention, combinatorially-derived variants are generated which have a selective potency relative to a naturally occurring ADAMTS13. Such proteins, when expressed from recombinant DNA constructs, can be used in gene therapy protocols.

Still other embodiments of the present invention provide ADAMTS13 variants that have intracellular half-lives dramatically different than the corresponding wild-type protein.

For example, the altered protein can be rendered either more stable or less stable to proteolytic degradation or other cellular process that result in destruction of, or otherwise inactivate ADAMTS13. Such variants, and the genes which encode them, can be utilized to alter the location of ADAMTS13 expression by modulating the half-life of the protein. For instance, a short half-life can give rise to more transient ADAMTS13 biological effects and, when part of an inducible expression system, can allow tighter control of ADAMTS13 levels within the cell. As above, such proteins, and particularly their recombinant nucleic acid constructs, can be used in gene therapy protocols.

In some embodiments of the combinatorial mutagenesis approach of the present invention, the amino acid sequences for a population of ADAMTS13 homologs, variants or other related proteins are aligned, preferably to promote the highest homology possible. Such a population of variants can include, for example, ADAMTS13 homologs from one or more species, or ADAMTS13 variants from the same species but which differ due to mutation or polymorphisms. Amino acids that appear at each position of the aligned sequences are selected to create a degenerate set of combinatorial sequences.

In a preferred embodiment of the present invention, the combinatorial ADAMTS13 library is produced by way of a degenerate library of genes encoding a library of polypeptides which each include at least a portion of potential ADAMTS13 protein sequences. For example, a mixture of synthetic oligonucleotides can be enzymatically ligated into gene sequences such that the degenerate set of potential ADAMTS13 sequences are expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of ADAMTS13 sequences therein.

There are many ways by which the library of potential ADAMTS13 homologs and variants can be generated from a degenerate oligonucleotide sequence. In some embodiments, chemical synthesis of a degenerate gene sequence is carried out in an automatic DNA synthesizer, and the synthetic genes are ligated into an appropriate gene for expression. The purpose of a degenerate set of genes is to provide, in one mixture, all of the sequences encoding the desired set of potential ADAMTS13 sequences. The synthesis of degenerate oligonucleotides is well known in the art (*See e.g.*, Narang (1983) Tetrahedron Lett., 39:39; Itakura *et al.* (1981) Recombinant DNA, *in* Walton (ed.), *Proceedings of the 3rd Cleveland Symposium on Macromolecules,* Elsevier, Amsterdam, pp 273-289; Itakura *et al.* (1984) Annu. Rev. Biochem., 53:323; Itakura *et al.* (1984) Science 198:1056; Ike *et al.* (1983) Nucl. Acid Res., 11:477). Such techniques have been employed in the directed evolution of other proteins (*See e.g.*, Scott *et al.* (1980) Science 249:386; Roberts *et al.*

(1992) Proc. Natl. Acad. Sci. USA 89:2429; Devlin *et al.* (1990) Science 249: 404; Cwirla *et al.* (1990) Proc. Natl. Acad. Sci. USA 87: 6378; as well as U.S. Pat. Nos. 5,223,409, 5,198,346, and 5,096,815; each of which is incorporated herein by reference).

It is contemplated that the ADAMTS13 encoding nucleic acids (*e.g.*, SEQ ID NO:1 and 3, and fragments and variants thereof) can be utilized as starting nucleic acids for directed evolution. These techniques can be utilized to develop ADAMTS13 variants having desirable properties such as increased or decreased specificity for VWF or other protein substrates.

In some embodiments, artificial evolution is performed by random mutagenesis (*e.g.*, by utilizing error-prone PCR to introduce random mutations into a given coding sequence). This method requires that the frequency of mutation be finely tuned. As a general rule, beneficial mutations are rare, while deleterious mutations are common. This is because the combination of a deleterious mutation and a beneficial mutation often results in an inactive enzyme. The ideal number of base substitutions for targeted gene is usually between 1.5 and 5 (Moore and Arnold (1996) Nat. Biotech., 14, 458; Leung *et al.* (1989) Technique, 1:11; Eckert and Kunkel (1991) PCR Methods Appl., 1:17-24; Caldwell and Joyce (1992) PCR Methods Appl., 2:28; and Zhao and Arnold (1997) Nuc. Acids. Res., 25:1307). After mutagenesis, the resulting clones are selected for desirable activity (*e.g.*, screened for ADAMTS13 activity). Successive rounds of mutagenesis and selection are often necessary to develop enzymes with desirable properties. It should be noted that only the useful mutations are carried over to the next round of mutagenesis.

In other embodiments of the present invention, the polynucleotides of the present invention are used in gene shuffling or sexual PCR procedures (*e.g.*, Smith (1994) Nature, 370:324; U.S. Pat. Nos. 5,837,458; 5,830,721; 5,811,238; 5,733,731; all of which are herein incorporated by reference). Gene shuffling involves random fragmentation of several mutant DNAs followed by their reassembly by PCR into full length molecules. Examples of various gene shuffling procedures include, but are not limited to, assembly following DNase treatment, the staggered extension process (STEP), and random priming in vitro recombination. In the DNase mediated method, DNA segments isolated from a pool of positive mutants are cleaved into random fragments with DNaseI and subjected to multiple rounds of PCR with no added primer. The lengths of random fragments approach that of the uncleaved segment as the PCR cycles proceed, resulting in mutations in present in different clones becoming mixed and accumulating in some of the resulting sequences. Multiple cycles of selection and shuffling have led to the functional enhancement of several

enzymes (Stemmer [1994] Nature, 370:398; Stemmer [1994] Proc. Natl. Acad. Sci. USA, 91:10747; Crameri *et al.* [1996] Nat. Biotech., 14:315; Zhang *et al.* [1997] Proc. Natl. Acad. Sci. USA, 94:4504; and Crameri *et al.* [1997] Nat. Biotech., 15:436). Variants produced by directed evolution can be screened for ADAMTS13 activity by the methods described in Example 1B.

A wide range of techniques are known in the art for screening gene products of combinatorial libraries made by point mutations, and for screening cDNA libraries for gene products having a certain property. Such techniques will be generally adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis or recombination of ADAMTS13 homologs or variants. The most widely used techniques for screening large gene libraries typically comprises cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates relatively easy isolation of the vector encoding the gene whose product was detected.

G. Chemical Synthesis of ADAMTS13

In an alternate embodiment of the invention, the coding sequence of ADAMTS13 is synthesized, whole or in part, using chemical methods well known in the art (*See e.g.*, Caruthers *et al.* (1980) Nucl. Acids Res. Symp. Ser., 7:215; Crea and Horn (1980) Nucl. Acids Res., 9:2331; Matteucci and Caruthers (1980) Tetrahedron Lett., 21:719; and Chow and Kempe (1981) Nucl. Acids Res., 9:2807). In other embodiments of the present invention, the protein itself is produced using chemical methods to synthesize either an entire ADAMTS13 amino acid sequence or a portion thereof. For example, peptides can be synthesized by solid phase techniques, cleaved from the resin, and purified by preparative high performance liquid chromatography (*See e.g.*, Creighton (1983) *Proteins Structures And Molecular Principles*, W H Freeman and Co, New York N.Y.). In other embodiments of the present invention, the composition of the synthetic peptides is confirmed by amino acid analysis or sequencing (*See e.g.*, Creighton, *supra*).

Direct peptide synthesis can be performed using various solid-phase techniques (Roberge *et al.* [1995] Science 269:202) and automated synthesis may be achieved, for example, using ABI 431A Peptide Synthesizer (Perkin Elmer) in accordance with the instructions provided by the manufacturer. Additionally, the amino acid sequence of ADAMTS13, or any part thereof, may be altered during direct synthesis and/or combined using chemical methods with other sequences to produce a variant polypeptide.

III. Detection of *ADAMTS13* Alleles

A. *ADAMTS13* Alleles

In some embodiments, the present invention includes alleles of *ADAMTS13* that increase a patient's susceptibility to TTP disease (*e.g.*, including, but not limited to, the mutations shown in Table 1). Analysis of naturally occurring human *ADAMTS13* alleles revealed that patients with increased susceptibility to TTP disease have a mutant *ADAMTS13* allele that, for example, result in a frameshift (a 26 bp deletion in exon 19, 2374-2399del, and a single A insertion in exon 27, 3769-3770insA), an in frame 23 amino acid insertion as result of a single splice mutation (1584+5>A), or a non-conservative amino acid substitution (286G>G, H96D; 304 C>T, R102C; 587C>T, T196I; 1193G>A, R398H; 1582A>G, R528G; 2074C>T; R692C; 2851T>G, C951G; 3070T>G, C1024G; 3638G>A, C1213Y). These patients all have greatly decreased levels of VWF-cleaving protease levels (see Figure 1).

The present invention is not limited to a particular mechanism of action. Indeed, an understanding of the mechanism of action is not necessary to practice the present invention. Nevertheless, it is contemplated that ADAMTS13 is involved in normal proteolytic processing of VWF. It is contemplated that in TTP the accumulation of hyperactive large VWF multimers in the absence of normal proteolytic processing triggers pathologic platelet aggregation and is the direct mechanism responsible for TTP.

However, the present invention is not limited to the mutations described in Table 1. Any mutation that results in the undesired phenotype (*e.g.*, a low level of VWF cleaving protease activity, or the presence of or susceptibility to TTP) is within the scope of the present invention. Assays for determining if a given polypeptide has a decreased level of VWF cleaving protease activity are provided in Example 1C.

For example, in some embodiments, the present invention provides alleles containing one or more single-nucleotide changes of *ADAMTS13* (*e.g.*, mutants or polymorphic sequences) (*e.g.*, including but not limited to the mutations shown in Table 1, and the polymorphisms shown in Table 2).

B. Detection of Variant Alleles

Accordingly, the present invention provides methods for determining whether a patient has an increased susceptibility to TTP disease by determining whether the individual

has a variant *ADAMTS13* allele. In other embodiments, the present invention provides methods for providing a prognosis of increased risk for TTP disease to an individual based on the presence or absence of one or more variant alleles of *ADAMTS13*. In preferred embodiments, the variation is a mutation resulting in decreased levels of VWF cleaving protease activity. In more preferred embodiments, the variation is a mutation described in Table 1.

A number of methods are available for analysis of variant (*e.g.*, mutant or polymorphic) nucleic acid sequences. Assays for detections polymorphisms or mutations fall into several categories, including, but not limited to direct sequencing assays, fragment polymorphism assays, hybridization assays, and computer based data analysis. Protocols and commercially available kits or services for performing multiple variations of these assays are available. In some embodiments, assays are performed in combination or in hybrid (*e.g.*, different reagents or technologies from several assays are combined to yield one assay). The following assays are useful in the present invention.

1. Direct Sequencing Assays

In some embodiments of the present invention, variant sequences are detected using a direct sequencing technique. In these assays, DNA samples are first isolated from a subject using any suitable method. In some embodiments, the region of interest is cloned into a suitable vector and amplified by growth in a host cell (*e.g.*, a bacteria). In other embodiments, DNA in the region of interest is amplified using PCR.

Following amplification, DNA in the region of interest (*e.g.*, the region containing the SNP or mutation of interest) is sequenced using any suitable method, including but not limited to manual sequencing using radioactive marker nucleotides, or automated sequencing. The results of the sequencing are displayed using any suitable method. The sequence is examined and the presence or absence of a given SNP or mutation is determined.

2. PCR Assays

In some embodiments of the present invention, variant sequences are detected using a PCR-based assay. In some embodiments, the PCR assay comprises the use of oligonucleotide primers that hybridize only to the variant or wild type allele of *ADAMTS13* (*e.g.*, to the region of polymorphism or mutation). Both sets of primers are used to amplify a sample of DNA. If only the mutant primers result in a PCR product, then the patient has the mutant *ADAMTS13* allele. If only the wild-type primers result in a PCR product, then the patient has the wild type allele of *ADAMTS13*.

3. Fragment Length Polymorphism Assays

In some embodiments of the present invention, variant sequences are detected using a fragment length polymorphism assay. In a fragment length polymorphism assay, a unique DNA banding pattern based on cleaving the DNA at a series of positions is generated using an enzyme (*e.g.*, a restriction enzyme or a CLEAVASE I [Third Wave Technologies, Madison, WI] enzyme). DNA fragments from a sample containing a SNP or a mutation will have a different banding pattern than wild type.

a. RFLP Assays

In some embodiments of the present invention, variant sequences are detected using a restriction fragment length polymorphism assay (RFLP). The region of interest is first isolated using PCR. The PCR products are then cleaved with restriction enzymes known to give a unique length fragment for a given polymorphism. The restriction-enzyme digested PCR products are separated by agarose gel electrophoresis and visualized by ethidium bromide staining. The length of the fragments is compared to molecular weight markers and fragments generated from wild-type and mutant controls.

b. CFLP assays

In other embodiments, variant sequences are detected using a CLEAVASE fragment length polymorphism assay (CFLP; Third Wave Technologies, Madison, WI; *See e.g.*, U.S. Patent Nos. 5,843,654; 5,843,669; 5,719,208; and 5,888,780; each of which is herein incorporated by reference). This assay is based on the observation that when single strands of DNA fold on themselves, they assume higher order structures that are highly individual to the precise sequence of the DNA molecule. These secondary structures involve partially duplexed regions of DNA such that single stranded regions are juxtaposed with double stranded DNA hairpins. The CLEAVASE I enzyme, is a structure-specific, thermostable nuclease that recognizes and cleaves the junctions between these single-stranded and double-stranded regions.

The region of interest is first isolated, for example, using PCR. Then, DNA strands are separated by heating. Next, the reactions are cooled to allow intrastrand secondary structure to form. The PCR products are then treated with the CLEAVASE I enzyme to generate a series of fragments that are unique to a given SNP or mutation. The CLEAVASE enzyme treated PCR products are separated and detected (*e.g.*, by agarose gel electrophoresis) and visualized (*e.g.*, by ethidium bromide staining). The length of the fragments is compared to molecular weight markers and fragments generated from wild-type and mutant controls.

4. Hybridization Assays

In preferred embodiments of the present invention, variant sequences are detected by hybridization analysis in a hybridization assay. In a hybridization assay, the presence of absence of a given SNP or mutation is determined based on the ability of the DNA from the sample to hybridize to a complementary DNA molecule (*e.g.*, a oligonucleotide probe). A variety of hybridization assays using a variety of technologies for hybridization and detection are available. A description of a selection of assays is provided below.

a. Direct Detection of Hybridization

In some embodiments, hybridization of a probe to the sequence of interest (*e.g.*, a SNP or mutation) is detected directly by visualizing a bound probe (*e.g.*, a Northern or Southern assay; *See e.g.*, Ausabel *et al.* (eds.) (1991) Current Protocols in Molecular Biology, John Wiley & Sons, NY). In a these assays, genomic DNA (Southern) or RNA (Northern) is isolated from a subject. The DNA or RNA is then cleaved with a series of restriction enzymes that cleave infrequently in the genome and not near any of the markers being assayed. The DNA or RNA is then separated (*e.g.*, on an agarose gel) and transferred to a membrane. A labeled (*e.g.*, by incorporating a radionucleotide) probe or probes specific for the SNP or mutation being detected is allowed to contact the membrane under a condition or low, medium, or high stringency conditions. Unbound probe is removed and the presence of binding is detected by visualizing the labeled probe.

b. Detection of Hybridization Using "DNA Chip" Assays

In some embodiments of the present invention, variant sequences are detected using a DNA chip hybridization assay. In this assay, a series of oligonucleotide probes are affixed to a solid support. The oligonucleotide probes are designed to be unique to a given SNP or mutation. The DNA sample of interest is contacted with the DNA "chip" and hybridization is detected.

In some embodiments, the DNA chip assay is a GeneChip (Affymetrix, Santa Clara, CA; *See e.g.*, U.S. Patent Nos. 6,045,996; 5,925,525; and 5,858,659; each of which is herein incorporated by reference) assay. The GeneChip technology uses miniaturized, high-density arrays of oligonucleotide probes affixed to a "chip." Probe arrays are manufactured by Affymetrix's light-directed chemical synthesis process, which combines solid-phase chemical synthesis with photolithographic fabrication techniques employed in the semiconductor industry. Using a series of photolithographic masks to define chip exposure sites, followed by specific chemical synthesis steps, the process constructs high-density arrays of oligonucleotides, with each probe in a predefined position in the

array. Multiple probe arrays are synthesized simultaneously on a large glass wafer. The wafers are then diced, and individual probe arrays are packaged in injection-molded plastic cartridges, which protect them from the environment and serve as chambers for hybridization.

The nucleic acid to be analyzed is isolated, amplified by PCR, and labeled with a fluorescent reporter group. The labeled DNA is then incubated with the array using a fluidics station. The array is then inserted into the scanner, where patterns of hybridization are detected. The hybridization data are collected as light emitted from the fluorescent reporter groups already incorporated into the target, which is bound to the probe array. Probes that perfectly match the target generally produce stronger signals than those that have mismatches. Since the sequence and position of each probe on the array are known, by complementarity, the identity of the target nucleic acid applied to the probe array can be determined.

In other embodiments, a DNA microchip containing electronically captured probes (Nanogen, San Diego, CA) is utilized (*See e.g.*, U.S. Patent Nos. 6,017,696; 6,068,818; and 6,051,380; each of which are herein incorporated by reference). Through the use of microelectronics, Nanogen's technology enables the active movement and concentration of charged molecules to and from designated test sites on its semiconductor microchip. DNA capture probes unique to a given SNP or mutation are electronically placed at, or "addressed" to, specific sites on the microchip. Since DNA has a strong negative charge, it can be electronically moved to an area of positive charge.

First, a test site or a row of test sites on the microchip is electronically activated with a positive charge. Next, a solution containing the DNA probes is introduced onto the microchip. The negatively charged probes rapidly move to the positively charged sites, where they concentrate and are chemically bound to a site on the microchip. The microchip is then washed and another solution of distinct DNA probes is added until the array of specifically bound DNA probes is complete.

A test sample is then analyzed for the presence of target DNA molecules by determining which of the DNA capture probes hybridize, with complementary DNA in the test sample (*e.g.*, a PCR amplified gene of interest). An electronic charge is also used to move and concentrate target molecules to one or more test sites on the microchip. The electronic concentration of sample DNA at each test site promotes rapid hybridization of sample DNA with complementary capture probes (hybridization may occur in minutes). To remove any unbound or nonspecifically bound DNA from each site, the polarity or charge

of the site is reversed to negative, thereby forcing any unbound or nonspecifically bound DNA back into solution away from the capture probes. A laser-based fluorescence scanner is used to detect binding,

In still further embodiments, an array technology based upon the segregation of fluids on a flat surface (chip) by differences in surface tension (ProtoGene, Palo Alto, CA) is utilized (*See e.g.*, U.S. Patent Nos. 6,001,311; 5,985,551; and 5,474,796; each of which is herein incorporated by reference). Protogene's technology is based on the fact that fluids can be segregated on a flat surface by differences in surface tension that have been imparted by chemical coatings. Once so segregated, oligonucleotide probes are synthesized directly on the chip by ink-jet printing of reagents. The array with its reaction sites defined by surface tension is mounted on a X/Y translation stage under a set of four piezoelectric nozzles, one for each of the four standard DNA bases. The translation stage moves along each of the rows of the array and the appropriate reagent is delivered to each of the reaction site. For example, the amidite A is delivered only to the sites where amidite A is to be coupled during that synthesis step and so on. Common reagents and washes are delivered by flooding the entire surface and then removing them by spinning.

DNA probes unique for the SNP or mutation of interest are affixed to the chip using Protogene's technology. The chip is then contacted with the PCR-amplified genes of interest. Following hybridization, unbound DNA is removed and hybridization is detected using any suitable method (*e.g.*, by fluorescence de-quenching of an incorporated fluorescent group).

In yet other embodiments, a "bead array" is used for the detection of polymorphisms (Illumina, San Diego, CA; *See e.g.*, PCT Publications WO 99/67641 and WO 00/39587, each of which is herein incorporated by reference). Illumina uses a BEAD ARRAY technology that combines fiber optic bundles and beads that self-assemble into an array. Each fiber optic bundle contains thousands to millions of individual fibers depending on the diameter of the bundle. The beads are coated with an oligonucleotide specific for the detection of a given SNP or mutation. Batches of beads are combined to form a pool specific to the array. To perform an assay, the BEAD ARRAY is contacted with a prepared subject sample (e.g., DNA). Hybridization is detected using any suitable method.

c. Enzymatic Detection of Hybridization

In some embodiments of the present invention, hybridization is detected by enzymatic cleavage of specific structures (INVADER assay, Third Wave Technologies; *See e.g.*, U.S. Patent Nos. 5,846,717, 6,090,543; 6,001,567; 5,985,557; and 5,994,069; each of

which is herein incorporated by reference). The INVADER assay detects specific DNA and RNA sequences by using structure-specific enzymes to cleave a complex formed by the hybridization of overlapping oligonucleotide probes. Elevated temperature and an excess of one of the probes enable multiple probes to be cleaved for each target sequence present without temperature cycling. These cleaved probes then direct cleavage of a second labeled probe. The secondary probe oligonucleotide can be 5'-end labeled with fluorescein that is quenched by an internal dye. Upon cleavage, the de-quenched fluorescein labeled product may be detected using a standard fluorescence plate reader.

The INVADER assay detects specific mutations and SNPs in unamplified genomic DNA. The isolated DNA sample is contacted with the first probe specific either for a SNP/mutation or wild type sequence and allowed to hybridize. Then a secondary probe, specific to the first probe, and containing the fluorescein label, is hybridized and the enzyme is added. Binding is detected by using a fluorescent plate reader and comparing the signal of the test sample to known positive and negative controls.

In some embodiments, hybridization of a bound probe is detected using a TaqMan assay (PE Biosystems, Foster City, CA; *See e.g.*, U.S. Patent Nos. 5,962,233 and 5,538,848, each of which is herein incorporated by reference). The assay is performed during a PCR reaction. The TaqMan assay exploits the 5'-3' exonuclease activity of the AMPLITAQ GOLD DNA polymerase. A probe, specific for a given allele or mutation, is included in the PCR reaction. The probe consists of an oligonucleotide with a 5'-reporter dye (*e.g.*, a fluorescent dye) and a 3'-quencher dye. During PCR, if the probe is bound to its target, the 5'-3' nucleolytic activity of the AMPLITAQ GOLD polymerase cleaves the probe between the reporter and the quencher dye. The separation of the reporter dye from the quencher dye results in an increase of fluorescence. The signal accumulates with each cycle of PCR and can be monitored with a fluorimeter.

In still further embodiments, polymorphisms are detected using the SNP-IT primer extension assay (Orchid Biosciences, Princeton, NJ; *See e.g.*, U.S. Patent Nos. 5,952,174 and 5,919,626, each of which is herein incorporated by reference). In this assay, SNPs are identified by using a specially synthesized DNA primer and a DNA polymerase to selectively extend the DNA chain by one base at the suspected SNP location. DNA in the region of interest is amplified and denatured. Polymerase reactions are then performed using miniaturized systems called microfluidics. Detection is accomplished by adding a label to the nucleotide suspected of being at the SNP or mutation location. Incorporation of

the label into the DNA can be detected by any suitable method (*e.g.*, if the nucleotide contains a biotin label, detection is via a fluorescently labeled antibody specific for biotin).

5. Mass Spectroscopy Assays

In some embodiments, a MassARRAY system (Sequenom, San Diego, CA.) is used to detect variant sequences (*See e.g.*, U.S. Patent Nos. 6,043,031; 5,777,324; and 5,605,798; each of which is herein incorporated by reference). DNA is isolated from blood samples using standard procedures. Next, specific DNA regions containing the mutation or SNP of interest, about 200 base pairs in length, are amplified by PCR. The amplified fragments are then attached by one strand to a solid surface and the non-immobilized strands are removed by standard denaturation and washing. The remaining immobilized single strand then serves as a template for automated enzymatic reactions that produce genotype specific diagnostic products.

Very small quantities of the enzymatic products, typically five to ten nanoliters, are then transferred to a SpectroCHIP array for subsequent automated analysis with the SpectroREADER mass spectrometer. Each spot is preloaded with light absorbing crystals that form a matrix with the dispensed diagnostic product. The MassARRAY system uses MALDI-TOF (Matrix Assisted Laser Desorption Ionization - Time of Flight) mass spectrometry. In a process known as desorption, the matrix is hit with a pulse from a laser beam. Energy from the laser beam is transferred to the matrix and it is vaporized resulting in a small amount of the diagnostic product being expelled into a flight tube. As the diagnostic product is charged, when an electrical field pulse is subsequently applied to the tube the diagnostic product is launched down the flight tube towards a detector. The time between application of the electrical field pulse and collision of the diagnostic product with the detector is referred to as the time of flight. This is a very precise measure of the product's molecular weight, as a molecule's mass correlates directly with time of flight with smaller molecules flying faster than larger molecules. The entire assay is completed in less than one thousandth of a second, enabling samples to be analyzed in a total of 3-5 second including repetitive data collection. The SpectroTYPER software then calculates, records, compares and reports the genotypes at the rate of three seconds per sample.

6. Variant Analysis by Differential Antibody Binding

In other embodiments of the present invention, antibodies (See below for antibody production) are used to determine if an individual contains an allele encoding an *ADAMTS13* gene containing a mutation. In preferred embodiments, antibodies are utilized

that discriminate between mutant (*i.e.*, truncated proteins); and wild-type proteins (SEQ ID NO:2).

7. Kits for Analyzing Risk of TTP Disease

The present invention also provides kits for determining whether an individual contains a wild-type or variant (*e.g.*, mutant or polymorphic) allele of *ADAMTS13*. In some embodiments, the kits are useful determining whether the subject is at risk of developing TTP disease. The diagnostic kits are produced in a variety of ways. In some embodiments, the kits contain at least one reagent for specifically detecting a mutant *ADAMTS13* allele or protein. In some preferred embodiments, the kits contain reagents for detecting a SNP caused by a single nucleotide substitution of the wild-type gene. In these preferred embodiments, the reagent is a nucleic acid that hybridizes to nucleic acids containing the SNP and that does not bind to nucleic acids that do not contain the SNP. In other preferred embodiments, the reagents are primers for amplifying the region of DNA containing the SNP. In still other embodiments, the reagents are antibodies that preferentially bind either the wild-type or mutant ADAMTS13 proteins. In some embodiments, the kit contains instructions for determining whether the subject is at risk for developing TTP disease. In preferred embodiments, the instructions specify that risk for developing TTP disease is determined by detecting the presence or absence of a mutant *ADAMTS13* allele in the subject, wherein subjects having an allele containing a single nucleotide substitution mutation have an increased risk of developing TTP disease. In some embodiments, the kits include ancillary reagents such as buffering agents, nucleic acid stabilizing reagents, protein stabilizing reagents, and signal producing systems (*e.g.*, florescence generating systems as Fret systems). The test kit may be packages in any suitable manner, typically with the elements in a single container or various containers as necessary along with a sheet of instructions for carrying out the test. In some embodiments, the kits also preferably include a positive control sample.

8. Bioinformatics

In some embodiments, the present invention provides methods of determining an individual's risk of developing TTP disease based on the presence of one or more variant alleles of *ADAMTS13*. In some embodiments, the analysis of variant data is processed by a computer using information stored on a computer (*e.g.*, in a database). For example, in some embodiments, the present invention provides a bioinformatics research system comprising a plurality of computers running a multi-platform object oriented programming language (*See e.g.*, U.S. Patent 6,125,383; herein incorporated by reference). In some

embodiments, one of the computers stores genetics data (*e.g.*, the risk of contacting TTP disease associated with a given polymorphism, as well as the sequences). Results are then delivered to the user (*e.g.*, via one of the computers or via the internet).

IV. Generation of ADAMTS13 Antibodies

Antibodies can be generated to allow for the detection of ADAMTS13 protein. The antibodies may be prepared using various immunogens. In one embodiment, the immunogen is anADAMTS13 peptide to generate antibodies that recognize human ADAMTS13. Such antibodies include, but are not limited to polyclonal, monoclonal, chimeric, single chain, Fab fragments, and Fab expression libraries.

Various procedures known in the art may be used for the production of polyclonal antibodies directed against ADAMTS13. For the production of antibody, various host animals can be immunized by injection with the peptide corresponding to the ADAMTS13 epitope including but not limited to rabbits, mice, rats, sheep, goats, etc. In a preferred embodiment, the peptide is conjugated to an immunogenic carrier (*e.g.*, diphtheria toxoid, bovine serum albumin (BSA), or keyhole limpet hemocyanin (KLH)). Various adjuvants may be used to increase the immunological response, depending on the host species, including but not limited to Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (Bacille Calmette-Guerin) and *Corynebacterium parvum*).

For preparation of monoclonal antibodies directed toward ADAMTS13, it is contemplated that any technique that provides for the production of antibody molecules by continuous cell lines in culture will find use with the present invention (*See e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press*, Cold Spring Harbor, NY). These include but are not limited to the hybridoma technique originally developed by Köhler and Milstein (Köhler & Milstein [1975] Nature 256:495-497), as well as the trioma technique, the human B-cell hybridoma technique (*See e.g.*, Kozbor *et al.* (1983) Immunol. Tod., 4:72), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole *et al.* [1985] *in Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-6).

In an additional embodiment of the invention, monoclonal antibodies are produced in germ-free animals utilizing technology such as that described in PCT/US90/02545).

Furthermore, it is contemplated that human antibodies will be generated by human hybridomas (Cote *et al.* [1983] Proc. Natl. Acad. Sci. USA 80:2026-2030) or by transforming human B cells with EBV virus *in vitro* (Cole *et al.* [1985] *in Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, pp. 77-96).

In addition, it is contemplated that techniques described for the production of single chain antibodies (U.S. Patent 4,946,778; herein incorporated by reference) will find use in producing ADAMTS13 specific single chain antibodies. An additional embodiment of the invention utilizes the techniques described for the construction of Fab expression libraries (Huse *et al.* [1989] Science 246:1275-1281) to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity for ADAMTS13.

It is contemplated that any technique suitable for producing antibody fragments will find use in generating antibody fragments that contain the idiotype (antigen binding region) of the antibody molecule. For example, such fragments include but are not limited to: F(ab')2 fragment that can be produced by pepsin digestion of the antibody molecule; Fab' fragments that can be generated by reducing the disulfide bridges of the F(ab')2 fragment, and Fab fragments that can be generated by treating the antibody molecule with papain and a reducing agent.

In the production of antibodies, it is contemplated that screening for the desired antibody will be accomplished by techniques known in the art (*e.g.*, radioimmunoassay, ELISA (enzyme-linked immunosorbant assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitation reactions, immunodiffusion assays, *in situ* immunoassays (*e.g.*, using colloidal gold, enzyme or radioisotope labels, for example), Western blots, precipitation reactions, agglutination assays (*e.g.*, gel agglutination assays, hemagglutination assays, etc.), complement fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, etc.

In one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labeled. Many means are known in the art for detecting binding in an immunoassay and are within the scope of the present invention. As is well known in the art, the immunogenic peptide should be provided free of the carrier molecule used in any immunization protocol. For example, if the peptide was conjugated to KLH, it may be conjugated to BSA, or used directly, in a screening assay.)

The foregoing antibodies can be used in methods known in the art relating to the localization and structure of ADAMTS13 (*e.g.*, for Western blotting), measuring levels thereof in appropriate biological samples, etc. The antibodies can be used to detect ADAMTS13 in a biological sample from an individual. The biological sample can be a biological fluid, such as, but not limited to, blood, serum, plasma, interstitial fluid, urine, cerebrospinal fluid, and the like, containing cells.

The biological samples can then be tested directly for the presence of ADAMTS13 using an appropriate strategy (*e.g.*, ELISA or radioimmunoassay) and format (*e.g.*, microwells, dipstick (*e.g.*, as described in International Patent Publication WO 93/03367), etc. Alternatively, proteins in the sample can be size separated (*e.g.*, by polyacrylamide gel electrophoresis (PAGE), in the presence or not of sodium dodecyl sulfate (SDS), and the presence of ADAMTS13 detected by immunoblotting (Western blotting). Immunoblotting techniques are generally more effective with antibodies generated against a peptide corresponding to an epitope of a protein, and hence, are particularly suited to the present invention.

In other embodiments, the antigen is a peptide fragment of ADAMTS13; preferably, the fragment is of high antigenicity. In yet other embodiment, the immunogen is a variant or mutant of ADAMTS13 peptide to generate antibodies that recognize the variant or mutant ADAMTS13. Such antibodies include, but are not limited to polyclonal, monoclonal, chimeric, single chain, Fab fragments, and Fab expression libraries, and are prepared and used as described above. These antibodies can then be used to detect the presence of a fragment or variant or mutant ADAMTS13 in a biological sample from an individual, as described above, and thus to predict the susceptibility of the individual to TTP.

For example, peptide antibodies have been synthesized against one peptide in exon 5 and one peptide in exon 13. These peptide fragments were selected on the basis of determinations by computer algorithms and other methods as having high "antigenicity" (likely to elicit an immune response); the selected peptides were then synthesized. The peptide fragments were injected into rabbits, and the rabbits periodically bled and boosted with the peptide antigen between bleeds. This serum was used as the source of the antibodies, while the serum before peptide injection was used as a negative control. The antibodies are affinity purified by passing the serum over a column composed of the peptide to purify only antibodies that bind the peptide. At least one of these antibodies in the unpurified state detects a protein of approximately the right size that is present in normal

plasma but not patient plasma. Antibodies are also prepared against other peptide fragments.

V. Methods of Treatment of TTP

A. Gene Therapy Using *ADAMTS13* Coding Sequences

The present invention also provides methods and compositions suitable for gene therapy to alter ADAMTS13 expression, production, or function. As described above, the present invention provides *ADAMTS13* genes and provides methods of obtaining *ADAMTS13* genes from different species. Thus, the methods described below are generally applicable across many species. In some embodiments, it is contemplated that the gene therapy is performed by providing a subject with a wild-type allele of *ADAMTS13* (*i.e.*, an allele that does not contain a mutation which results in a decrease of VWF-cleaving protease activity; examples of such mutations are shown in Table 2). Subjects in need of such therapy are identified by the methods described above.

Viral vectors commonly used for *in vivo* or *ex vivo* targeting and therapy procedures are DNA-based vectors and retroviral vectors. Methods for constructing and using viral vectors are known in the art (*See e.g.* (1992) Miller and Rosman, BioTech., 7:980-990). Preferably, the viral vectors are replication defective, that is, they are unable to replicate autonomously in the target cell. In general, the genome of the replication defective viral vectors that are used within the scope of the present invention lack at least one region that is necessary for the replication of the virus in the infected cell. These regions can either be eliminated (in whole or in part), or be rendered non-functional by any technique known to a person skilled in the art. These techniques include the total removal, substitution (by other sequences, in particular by the inserted nucleic acid), partial deletion or addition of one or more bases to an essential (for replication) region. Such techniques may be performed *in vitro* (*i.e.*, on the isolated DNA) or *in situ*, using the techniques of genetic manipulation or by treatment with mutagenic agents.

Preferably, the replication defective virus retains the sequences of its genome that are necessary for encapsidating the viral particles. DNA viral vectors include an attenuated or defective DNA viruses, including, but not limited to, herpes simplex virus (HSV), papillomavirus, Epstein Barr virus (EBV), adenovirus, adeno-associated virus (AAV), and the like. Defective viruses, that entirely or almost entirely lack viral genes, are preferred, as defective virus is not infective after introduction into a cell. Use of defective viral vectors

allows for administration to cells in a specific, localized area, without concern that the vector can infect other cells. Thus, a specific tissue can be specifically targeted. Examples of particular vectors include, but are not limited to, a defective herpes virus 1 (HSV1) vector (Kaplitt *et al.* [1991] Mol. Cell. Neurosci., 2:320-330), defective herpes virus vector lacking a glycoprotein L gene (*See e.g.,* Patent Publication RD 371005 A), or other defective herpes virus vectors (*See e.g.,* WO 94/21807; and WO 92/05263); an attenuated adenovirus vector, such as the vector described by Stratford-Perricaudet *et al.* (J. Clin. Invest., 90:626-630 [1992]; *See also,* La Salle *et al.* [1993] Science 259:988-990); and a defective adeno-associated virus vector (Samulski *et al.* [1987] J. Virol., 61:3096-3101; Samulski *et al.* [1989] J. Virol., 63:3822-3828; and Lebkowski *et al.* [1988] Mol. Cell. Biol., 8:3988-3996).

Preferably, for *in vivo* administration, an appropriate immunosuppressive treatment is employed in conjunction with the viral vector (*e.g.,* adenovirus vector), to avoid immuno-deactivation of the viral vector and transfected cells. For example, immunosuppressive cytokines, such as interleukin-12 (IL-12), interferon-gamma (IFN-γ), or anti-CD4 antibody, can be administered to block humoral or cellular immune responses to the viral vectors. In addition, it is advantageous to employ a viral vector that is engineered to express a minimal number of antigens.

In a preferred embodiment, the vector is an adenovirus vector. Adenoviruses are eukaryotic DNA viruses that can be modified to efficiently deliver a nucleic acid of the invention to a variety of cell types. The present invention contemplates adenoviruses of both human and animal origin. (*See e.g.,* WO94/26914). Various serotypes of adenovirus exist. Those adenoviruses of animal origin that can be used within the scope of the present invention include adenoviruses of canine, bovine, murine (*e.g.,* Mav1, Beard *et al.* (1990) Virol., 75-81), ovine, porcine, avian, and simian (*e.g.,* SAV) origin. Preferably, the adenovirus of animal origin is a canine adenovirus, more preferably a CAV2 adenovirus (*e.g.* Manhattan or A26/61 strain (ATCC VR-800)).

Preferably, the replication defective adenoviral vectors of the invention comprise the ITRs, an encapsidation sequence and the nucleic acid of interest. Still more preferably, at least the E1 region of the adenoviral vector is non-functional. The deletion in the E1 region preferably extends from nucleotides 455 to 3329 in the sequence of the Ad5 adenovirus (*Pvu*II-*Bgl*II fragment) or 382 to 3446 (*Hin*fII-*Sau*3A fragment). Other regions may also be modified, in particular the E3 region (*e.g.,* WO95/02697), the E2 region (*e.g.,* WO94/28938), the E4 region (*e.g.,* WO94/28152, WO94/12649 and WO95/02697), or in any of the late genes L1-L5.

In a preferred embodiment, the adenoviral vector has a deletion in the E1 region (Ad 1.0). Examples of E1-deleted adenoviruses are disclosed in EP 185,573, the contents of which are incorporated herein by reference. In another preferred embodiment, the adenoviral vector has a deletion in the E1 and E4 regions (Ad 3.0). Examples of E1/E4-deleted adenoviruses are disclosed in WO95/02697 and WO96/22378. In still another preferred embodiment, the adenoviral vector has a deletion in the E1 region into which the E4 region and the nucleic acid sequence are inserted.

The replication defective recombinant adenoviruses according to the invention can be prepared by any technique known to the person skilled in the art (*See e.g.*, Levrero *et al.* (1991) Gene 101:195; EP 185 573; and Graham (1984) EMBO J., 3:2917). In particular, they can be prepared by homologous recombination between an adenovirus and a plasmid that carries, *inter alia*, the DNA sequence of interest. The homologous recombination is accomplished following co-transfection of the adenovirus and plasmid into an appropriate cell line. The cell line that is employed should preferably (i) be transformable by the elements to be used, and (ii) contain the sequences that are able to complement the part of the genome of the replication defective adenovirus, preferably in integrated form in order to avoid the risks of recombination. Examples of cell lines that may be used are the human embryonic kidney cell line 293 (Graham *et al.* [1977] J. Gen. Virol., 36:59), which contains the left-hand portion of the genome of an Ad5 adenovirus (12%) integrated into its genome, and cell lines that are able to complement the E1 and E4 functions, as described in applications WO94/26914 and WO95/02697. Recombinant adenoviruses are recovered and purified using standard molecular biological techniques that are well known to one of ordinary skill in the art.

The adeno-associated viruses (AAV) are DNA viruses of relatively small size that can integrate, in a stable and site-specific manner, into the genome of the cells that they infect. They are able to infect a wide spectrum of cells without inducing any effects on cellular growth, morphology or differentiation, and they do not appear to be involved in human pathologies. The AAV genome has been cloned, sequenced and characterized. It encompasses approximately 4700 bases and contains an inverted terminal repeat (ITR) region of approximately 145 bases at each end, which serves as an origin of replication for the virus. The remainder of the genome is divided into two essential regions that carry the encapsidation functions: the left-hand part of the genome, that contains the *rep* gene involved in viral replication and expression of the viral genes; and the right-hand part of the genome, that contains the *cap* gene encoding the capsid proteins of the virus.

The use of vectors derived from the AAVs for transferring genes *in vitro* and *in vivo* has been described (*See e.g.*, WO 91/18088; WO 93/09239; US Pat. No. 4,797,368; US Pat. No., 5,139,941; and EP 488 528, all of which are herein incorporated by reference). These publications describe various AAV-derived constructs in which the *rep* and/or *cap* genes are deleted and replaced by a gene of interest, and the use of these constructs for transferring the gene of interest *in vitro* (into cultured cells) or *in vivo* (directly into an organism). The replication defective recombinant AAVs according to the invention can be prepared by co-transfecting a plasmid containing the nucleic acid sequence of interest flanked by two AAV inverted terminal repeat (ITR) regions, and a plasmid carrying the AAV encapsidation genes (*rep* and *cap* genes), into a cell line that is infected with a human helper virus (for example an adenovirus). The AAV recombinants that are produced are then purified by standard techniques.

In another embodiment, the gene can be introduced in a retroviral vector (*e.g.*, as described in U.S. Pat. Nos. 5,399,346, 4,650,764, 4,980,289 and 5,124,263; all of which are herein incorporated by reference; Mann *et al.* (1983) Cell 33:153; Markowitz *et al.* (1988) J. Virol., 62:1120; PCT/US95/14575; EP 453242; EP178220; Bernstein *et al.* (1985) Genet. Eng., 7:235; McCormick, (1985) BioTechnol., 3:689; WO 95/07358; and Kuo *et al.*, (1993) :845). The retroviruses are integrating viruses that infect dividing cells. The retrovirus genome includes two LTRs, an encapsidation sequence and three coding regions (*gag, pol* and *env*). In recombinant retroviral vectors, the *gag, pol* and *env* genes are generally deleted, in whole or in part, and replaced with a heterologous nucleic acid sequence of interest. These vectors can be constructed from different types of retrovirus, such as, HIV, MoMuLV ("murine Moloney leukaemia virus" MSV ("murine Moloney sarcoma virus"), HaSV ("Harvey sarcoma virus"); SNV ("spleen necrosis virus"); RSV ("Rous sarcoma virus") and Friend virus. Defective retroviral vectors are also disclosed in WO95/02697.

In general, in order to construct recombinant retroviruses containing a nucleic acid sequence, a plasmid is constructed that contains the LTRs, the encapsidation sequence and the coding sequence. This construct is used to transfect a packaging cell line, which cell line is able to supply in trans the retroviral functions that are deficient in the plasmid. In general, the packaging cell lines are thus able to express the *gag, pol* and *env* genes. Such packaging cell lines have been described in the prior art, in particular the cell line PA317 (US Pat. No. 4,861,719, herein incorporated by reference), the PsiCRIP cell line (*See,* WO90/02806), and the GP+envAm-12 cell line (*See,* WO89/07150). In addition, the recombinant retroviral vectors can contain modifications within the LTRs for suppressing

transcriptional activity as well as extensive encapsidation sequences that may include a part of the *gag* gene (Bender *et al.* [1987] Virol., 61:1639). Recombinant retroviral vectors are purified by standard techniques known to those having ordinary skill in the art.

Alternatively, the vector can be introduced *in vivo* by lipofection. For the past decade, there has been increasing use of liposomes for encapsulation and transfection of nucleic acids *in vitro*. Synthetic cationic lipids designed to limit the difficulties and dangers encountered with liposome mediated transfection can be used to prepare liposomes for *in vivo* transfection of a gene encoding a marker (Felgner *et. al.* [1987] Proc. Natl. Acad. Sci. USA 84:7413-7417; *See also,* Mackey, *et al.* (1988) Proc. Natl. Acad. Sci. USA 85:8027-8031; Ulmer *et al.* (1993) Science 259:1745-1748). The use of cationic lipids may promote encapsulation of negatively charged nucleic acids, and also promote fusion with negatively charged cell membranes (Felgner and Ringold [1989] Science 337:387-388). Particularly useful lipid compounds and compositions for transfer of nucleic acids are described in WO95/18863 and WO96/17823, and in U.S. Pat. No. 5,459,127, herein incorporated by reference.

Other molecules are also useful for facilitating transfection of a nucleic acid *in vivo*, such as a cationic oligopeptide (*e.g.*, WO95/21931), peptides derived from DNA binding proteins (*e.g.*, WO96/25508), or a cationic polymer (*e.g.*, WO95/21931).

It is also possible to introduce the vector *in vivo* as a naked DNA plasmid. Methods for formulating and administering naked DNA to mammalian muscle tissue are disclosed in U.S. Pat. Nos. 5,580,859 and 5,589,466, both of which are herein incorporated by reference.

DNA vectors for gene therapy can be introduced into the desired host cells by methods known in the art, including but not limited to transfection, electroporation, microinjection, transduction, cell fusion, DEAE dextran, calcium phosphate precipitation, use of a gene gun, or use of a DNA vector transporter (*See e.g.*, Wu *et al.* (1992) J. Biol. Chem., 267:963; Wu and Wu (1988) J. Biol. Chem., 263:14621; and Williams *et al.* (1991) Proc. Natl. Acad. Sci. USA 88:2726). Receptor-mediated DNA delivery approaches can also be used (Curiel *et al.* [1992] Hum. Gene Ther., 3:147; and Wu & Wu [1987] J. Biol. Chem., 262:4429).

B. Administration of ADAMTS13 Polypeptides

The present invention also provides methods and compositions suitable for administering ADAMTS13 to a patient suffering from TTP. As described above, the present invention provides nucleotides encoding ADAMTS13 and fragments, mutants, variants, and fusions thereof, and methods of producing the encoded polypeptides. The methods described below are generally applicable across many species.

In some embodiments, the invention provides a composition comprising purified ADAMTS13 peptides; in other embodiments, the invention provides a composition comprising purified ADAMTS13 polypeptide fragments, mutants, variants, or fusions, all of which possess the biological activity of ADAMTS13. Fragments, mutants, variants, or fusions may be used as necessary to alter characteristics of ADAMTS13 to improve its performance as a therapeutic treatment of TTP. Such characteristics include stability during storage and administration, circulating half-life, levels of activity, substrate specificity, localization to a particular tissue, and interaction with other molecules, such as receptors or enzymatic complexes. For example, the protein is preferably engineered to have a very long circulating half life. Such characteristics can be introduced as described above. The polypeptides can be produced as described above. The compositions are formulated as described.

In other embodiments, the invention provides a method of treating a patient with TTP disease, which comprises administering a therapeutically effective amount of ADAMTS13 such that symptoms of the disease are alleviated. As is well known in the medical arts, dosages for any one patient depends upon many factors, including the patient's size, body surface area, age, the particular compound to be administered, sex, time and route of administration, general health, and interaction with other drugs being concurrently administered. Although any method of administration is anticipated, as described further below, preferably the polypeptide is administered intravenously.

VI. Drug Screening Using ADAMTS13

The present invention provides methods and compositions for using ADAMTS13 as a target for screening drugs that can alter, for example, VWF-cleaving protease activity and associated symptoms (*e.g.*, TTP disease). For example, drugs that induce or inhibit VWF-cleaving protease activity can be identified by screening for compounds that target ADAMTS13 or regulate *ADAMTS13* gene expression.

The present invention is not limited to a particular mechanism of action. Indeed, an understanding of the mechanism of action is not necessary to practice the present invention. Nevertheless, it is contemplated that a decrease of VWF-cleaving protease activity leads to an accumulation of hyperactive large VWF multimers which triggers pathologic platelet aggregation and is the direct mechanism responsible for TTP. Thus, it is contemplated that drugs which induce VWF-cleaving protease activity can be used to prevent symptoms of TTP.

Alternatively, it is also contemplated that increased VWF-cleaving protease activity could also be used in normal individuals as a novel approach to anticoagulation (preventing abnormal blood clots). Since blood clots are at the basis of many important human diseases including heart attack and stroke, this new insight could be critical to the development of new pharmaceuticals to treat these very common human diseases as well as the rare disorder TTP. Such increased VWF-cleaving activity could be achieved by inducing the enzyme activity as described above. Other embodiments contemplate drugs based upon variants of the ADAMTS13 protease itself. Such proteases would, for example, be effective at reducing clots, be easily administered, and have a life span of sufficient duration as to treat the disease, but not to cause subsequent harm.

In one screening method, candidate compounds are evaluated for their ability to alter VWF-cleaving protease activity by adding the compound in the presence of an ADAMTS13 protease to an assay for the VWF-cleaving protease activity, for example as is described in Example 1B, and determining the effects of the compound on the level of protease activity.

In another screening method, variants of ADAMTS13 are evaluated for their ability to cleave VWF by adding the variants to an assay for the VWF-cleaving protease activity, for example as is described in Example 1B, and determining the level of protease activity of the variant.

Another technique uses ADAMTS13 antibodies, generated as discussed above. Such antibodies capable of specifically binding to ADAMTS13 peptides can be used to detect the presence of any peptide that shares one or more antigenic determinants of the ADAMTS13 peptide. Such peptides can then be evaluated for protease activity as described above.

The present invention contemplates many other means of screening compounds. The examples provided above are presented merely to illustrate a range of techniques available. One of ordinary skill in the art will appreciate that many other screening methods can be used.

In particular, the present invention contemplates the use of cell lines transfected with ADAMTS13 and variants thereof for screening compounds for activity, and in particular to high throughput screening of compounds from combinatorial libraries (*e.g.*, libraries containing greater than 10^4 compounds). The cell lines of the present invention can be used in a variety of screening methods. In some embodiments, the cells can be used in reporter gene assays that monitor cellular responses at the transcription/translation level. In still further embodiments, the cells can be used in cell proliferation assays to monitor the overall growth/no growth response of cells to external stimuli.

The cells are useful in reporter gene assays. Reporter gene assays involve the use of host cells transfected with vectors encoding a nucleic acid comprising transcriptional control elements of a target gene (*i.e.*, a gene that controls the biological expression and function of a disease target) spliced to a coding sequence for a reporter gene. Therefore, activation of the target gene results in activation of the reporter gene product. Examples of reporter genes finding use in the present invention include, but are not limited to, chloramphenicol transferase, alkaline phosphatase, firefly and bacterial luciferases, β-galactosidase, β-lactamase, and green fluorescent protein. The production of these proteins, with the exception of green fluorescent protein, is detected through the use of chemiluminescent, colorimetric, or bioluminescent products of specific substrates (*e.g.*, X-gal and luciferin). Comparisons between compounds of known and unknown activities may be conducted as described above.

VII. Pharmaceutical Compositions Containing ADAMTS13 Nucleotides, Peptides, and Antibodies, and Analogs

The present invention further provides pharmaceutical compositions which may comprise all or portions of ADAMTS13 encoding polynucleotide sequences, ADAMTS13 polypeptides, inhibitors or antagonists of ADAMTS13 bioactivity, including antibodies, alone or in combination with at least one other agent, such as a stabilizing compound, and may be administered in any sterile, biocompatible pharmaceutical carrier, including, but not limited to, saline, buffered saline, dextrose, and water.

The methods of the present invention find use in treating diseases or altering physiological states characterized by decreased VWF-cleaving protease activity, and/or pathologic platelet aggregation. The invention provides methods for increasing VWF-cleaving protease activity and/or decreasing pathologic platelet aggregation by administering peptides or peptide fragments or variants of ADAMTS13. Alternatively,

drugs which act to increase VWF-cleaving protease activity and/or decreasing pathologic platelet aggregation, as discovered through screening methods described above, are administered.

Peptides can be administered to the patient intravenously in a pharmaceutically acceptable carrier such as physiological saline. Standard methods for intracellular delivery of peptides can be used (*e.g.*, delivery via liposome). Such methods are well known to those of ordinary skill in the art. The formulations of this invention are useful for parenteral administration, such as intravenous, subcutaneous, intramuscular, and intraperitoneal. Therapeutic administration of a polypeptide intracellularly can also be accomplished using gene therapy as described above.

As is well known in the medical arts, dosages for any one patient depends upon many factors, including the patient's size, body surface area, age, the particular compound to be administered, sex, time and route of administration, general health, and interaction with other drugs being concurrently administered.

Accordingly, in some embodiments of the present invention, ADATS13 nucleotides and ADAMTS13 amino acid sequences can be administered to a patient alone, or in combination with other nucleotide sequences, drugs or hormones or in pharmaceutical compositions where it is mixed with excipient(s) or other pharmaceutically acceptable carriers. In one embodiment of the present invention, the pharmaceutically acceptable carrier is pharmaceutically inert. In another embodiment of the present invention, ADAMTS13 encoding polynucleotide sequences or ADAMTS13 amino acid sequences may be administered alone to individuals subject to or suffering from a disease, such as TTP or stroke.

Depending on the condition being treated, these pharmaceutical compositions may be formulated and administered systemically or locally. Techniques for formulation and administration may be found in the latest edition of "Remington's Pharmaceutical Sciences" (Mack Publishing Co, Easton Pa.). Suitable routes may, for example, include oral or transmucosal administration; as well as parenteral delivery, including intramuscular, subcutaneous, intramedullary, intrathecal, intraventricular, intravenous, intraperitoneal, or intranasal administration.

For injection, the pharmaceutical compositions of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiologically buffered saline. For tissue or cellular

administration, penetrants appropriate to the particular barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

In other embodiments, the pharmaceutical compositions of the present invention can be formulated using pharmaceutically acceptable carriers well known in the art in dosages suitable for oral administration. Such carriers enable the pharmaceutical compositions to be formulated as tablets, pills, capsules, liquids, gels, syrups, slurries, suspensions and the like, for oral or nasal ingestion by a patient to be treated.

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. For example, an effective amount of ADAMTS13 may be that amount that results in VWF-cleaving protease activity, or decreased levels of platelet aggregation, comparable to normal individuals who are not suffering from TTP or stroke. Determination of effective amounts is well within the capability of those skilled in the art, especially in light of the disclosure provided herein.

In addition to the active ingredients these pharmaceutical compositions may contain suitable pharmaceutically acceptable carriers comprising excipients and auxiliaries that facilitate processing of the active compounds into preparations which can be used pharmaceutically. The preparations formulated for oral administration may be in the form of tablets, dragees, capsules, or solutions.

The pharmaceutical compositions of the present invention may be manufactured in a manner that is itself known (*e.g.*, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes).

Pharmaceutical formulations for parenteral administration include aqueous solutions of the active compounds in water-soluble form. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Aqueous injection suspensions may contain substances that increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers or agents that increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

Pharmaceutical preparations for oral use can be obtained by combining the active compounds with solid excipient, optionally grinding a resulting mixture, and processing the

mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are carbohydrate or protein fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; starch from corn, wheat, rice, potato, etc; cellulose such as methyl cellulose, hydroxypropylmethyl-cellulose, or sodium carboxymethylcellulose; and gums including arabic and tragacanth; and proteins such as gelatin and collagen. If desired, disintegrating or solubilizing agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, alginic acid or a salt thereof such as sodium alginate.

Dragee cores are provided with suitable coatings such as concentrated sugar solutions, which may also contain gum arabic, talc, polyvinylpyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for product identification or to characterize the quantity of active compound, (*i.e.*, dosage).

Pharmaceutical preparations that can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a coating such as glycerol or sorbitol. The push-fit capsules can contain the active ingredients mixed with a filler or binders such as lactose or starches, lubricants such as talc or magnesium stearate, and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycol with or without stabilizers.

Compositions comprising a compound of the invention formulated in a pharmaceutical acceptable carrier may be prepared, placed in an appropriate container, and labeled for treatment of an indicated condition. For polynucleotide or amino acid sequences of ADAMTS13, conditions indicated on the label may include treatment of condition related to apoptosis.

The pharmaceutical composition may be provided as a salt and can be formed with many acids, including but not limited to hydrochloric, sulfuric, acetic, lactic, tartaric, malic, succinic, *etc.* Salts tend to be more soluble in aqueous or other protonic solvents that are the corresponding free base forms. In other cases, the preferred preparation may be a lyophilized powder in 1 mM-50 mM histidine, 0.1%-2% sucrose, 2%-% mannitol at a pH range of 4.5 to 5.5 that is combined with buffer prior to use.

For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. Then, preferably, dosage can be

formulated in animal models (particularly murine models) to achieve a desirable circulating concentration range that adjusts ADAMTS13 levels.

A therapeutically effective dose refers to that amount of ADAMTS13 or variant or drug that ameliorates symptoms of the disease state. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index, and it can be expressed as the ratio LD_{50}/ED_{50}. Compounds that exhibit large therapeutic indices are preferred. The data obtained from these cell culture assays and additional animal studies can be used in formulating a range of dosage for human use. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, sensitivity of the patient, and the route of administration.

The exact dosage is chosen by the individual physician in view of the patient to be treated. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Additional factors which may be taken into account include the severity of the disease state; age, weight, and gender of the patient; diet, time and frequency of administration, drug combination(s), reaction sensitivities, and tolerance/response to therapy. Long acting pharmaceutical compositions might be administered every 3 to 4 days, every week, or once every two weeks depending on half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from 0.1 to 100,000 micrograms, up to a total dose of about 1 g, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature (*See*, U.S. Pat. Nos. 4,657,760; 5,206,344; or 5,225,212, all of which are herein incorporated by reference). Those skilled in the art will employ different formulations for ADAMTS than for the inducers or enhancers of ADAMTS13. Administration to the bone marrow may necessitate delivery in a manner different from intravenous injections.

VIII. Transgenic Animals Expressing Exogenous *ADAMTS13* Genes and Homologs, Mutants, and Variants Thereof

The present invention contemplates the generation of transgenic animals comprising an exogenous *ADAMTS13* gene or homologs, mutants, or variants thereof. In preferred embodiments, the transgenic animal displays an altered phenotype as compared to wild-type animals. In some embodiments, the altered phenotype is the overexpression of mRNA for an *ADAMTS13* gene as compared to wild-type levels of *ADAMTS13* expression. In other embodiments, the altered phenotype is the decreased expression of mRNA for an endogenous *ADAMTS13* gene as compared to wild-type levels of endogenous *ADAMTS13* expression. In other embodiments, the transgenic mice have a knock out mutation of the *ADAMTS13* gene. In still further embodiments, the altered phenotype is expression of an *ADAMTS13* mutant gene; non-limiting examples of such mutants are shown in Table 1. In preferred embodiments, the transgenic animals display a TTP disease phenotype. Methods for analyzing the presence or absence of such altered phenotypes include Northern blotting, mRNA protection assays, RT-PCR, detection of protein expression with antibodies, and detection of protein activity with VWF-cleaving protease activity, such as is described in Example 1B.

The transgenic animals of the present invention find use in drug and treatment regime screens. In some embodiments, test compounds (*e.g.*, a drug that is suspected of being useful to treat TTP disease) and control compounds (*e.g.*, a placebo) are administered to the transgenic animals and the control animals and the effects evaluated. The effects of the test and control compounds on disease symptoms are then assessed.

The transgenic animals can be generated via a variety of methods. In some embodiments, embryonic cells at various developmental stages are used to introduce transgenes for the production of transgenic animals. Different methods are used depending on the stage of development of the embryonic cell. The zygote is the best target for micro-injection. In the mouse, the male pronucleus reaches the size of approximately 20 micrometers in diameter which allows reproducible injection of 1-2 picoliters (pl) of DNA solution. The use of zygotes as a target for gene transfer has a major advantage in that in most cases the injected DNA will be incorporated into the host genome before the first cleavage (Brinster *et al.* [1985] Proc. Natl. Acad. Sci. USA, 82:4438-4442). As a consequence, all cells of the transgenic non-human animal will carry the incorporated transgene. This will in general also be reflected in the efficient transmission of the transgene to offspring of the founder since 50% of the germ cells will harbor the transgene.

U.S. Patent No. 4,873,191 describes a method for the micro-injection of zygotes; the disclosure of this patent is incorporated herein in its entirety.

In other embodiments, retroviral infection is used to introduce transgenes into a non-human animal. In some embodiments, the retroviral vector is utilized to transfect oocytes by injecting the retroviral vector into the perivitelline space of the oocyte (U.S. Pat. No. 6,080,912, incorporated herein by reference). In other embodiments, the developing non-human embryo can be cultured *in vitro* to the blastocyst stage. During this time, the blastomeres can be targets for retroviral infection (Janenich [1976] Proc. Natl. Acad. Sci. USA, 73:1260). Efficient infection of the blastomeres is obtained by enzymatic treatment to remove the zona pellucida (Hogan *et al.* [1986] in *Manipulating the Mouse Embryo*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.). The viral vector system used to introduce the transgene is typically a replication-defective retrovirus carrying the transgene (Jahner *et al.* [1985] Proc. Natl. Acad Sci. USA 82:6927). Transfection is easily and efficiently obtained by culturing the blastomeres on a monolayer of virus-producing cells (Van der Putten, *supra*; Stewart, *et al.* [1987] EMBO J., 6:383). Alternatively, infection can be performed at a later stage. Virus or virus-producing cells can be injected into the blastocoele (Jahner *et al.* [1982] Nature 298:623). Most of the founders will be mosaic for the transgene since incorporation occurs only in a subset of cells that form the transgenic animal. Further, the founder may contain various retroviral insertions of the transgene at different positions in the genome that generally will segregate in the offspring. In addition, it is also possible to introduce transgenes into the germline, albeit with low efficiency, by intrauterine retroviral infection of the midgestation embryo (Jahner *et al.* [1982] supra). Additional means of using retroviruses or retroviral vectors to create transgenic animals known to the art involves the micro-injection of retroviral particles or mitomycin C-treated cells producing retrovirus into the perivitelline space of fertilized eggs or early embryos (PCT International Application WO 90/08832 [1990], and Haskell and Bowen (1995) Mol. Reprod. Dev., 40:386).

In other embodiments, the transgene is introduced into embryonic stem cells and the transfected stem cells are utilized to form an embryo. ES cells are obtained by culturing pre-implantation embryos *in vitro* under appropriate conditions (Evans *et al.* [1981] Nature 292:154; Bradley *et al.* [1984] Nature 309:255; Gossler *et al.* [1986] Proc. Acad. Sci. USA 83:9065; and Robertson *et al.* [1986] Nature 322:445). Transgenes can be efficiently introduced into the ES cells by DNA transfection by a variety of methods known to the art including calcium phosphate co-precipitation, protoplast or spheroplast fusion, lipofection

and DEAE-dextran-mediated transfection. Transgenes may also be introduced into ES cells by retrovirus-mediated transduction or by micro-injection. Such transfected ES cells can thereafter colonize an embryo following their introduction into the blastocoele of a blastocyst-stage embryo and contribute to the germ line of the resulting chimeric animal (for review, *See*, Jaenisch (1988) Science 240:1468). Prior to the introduction of transfected ES cells into the blastocoele, the transfected ES cells may be subjected to various selection protocols to enrich for ES cells which have integrated the transgene assuming that the transgene provides a means for such selection. Alternatively, the polymerase chain reaction may be used to screen for ES cells that have integrated the transgene. This technique obviates the need for growth of the transfected ES cells under appropriate selective conditions prior to transfer into the blastocoele.

In still other embodiments, homologous recombination is utilized knock-out gene function or create deletion mutants. Methods for homologous recombination are described in U.S. Pat. No. 5,614,396, incorporated herein by reference.

EXPERIMENTAL

The following examples are provided in order to demonstrate and further illustrate certain preferred embodiments and aspects of the present invention and are not to be construed as limiting the scope thereof.

In the experimental disclosure which follows, the following abbreviations apply: N (normal); M (molar); mM (millimolar); μM (micromolar); mol (moles); mmol (millimoles); μmol (micromoles); nmol (nanomoles); pmol (picomoles); g (grams); mg (milligrams); μg (micrograms); ng (nanograms); l or L (liters); ml or mL (milliliters); μl or μL (microliters); cm (centimeters); mm (millimeters); μm (micrometers); nm (nanometers); DS (dextran sulfate); °C (degrees Centigrade); U (units); ADAM (a disintegrin and metalloproteinase); TPP (thrombotic thrombocytopenic purpura); TSP (thrombospondin); von Wildebrandt factor (VWF) and Sigma (Sigma Chemical Co., St. Louis, MO).

EXAMPLE 1

Methods

This example describes the methods used to identify and characterize the gene *ADAMTS13*.

A. Subjects. Patients included in this study were referred for evaluation of thrombocytopenia, hemolytic anemia, and schistocytes on blood smear. Probands for the 4 families (A-D) used in the linkage analysis all had a chronic relapsing course, responded to plasma infusion, and had the disorder as neonates or had a family member with such a disorder as a neonate. The additional probands studied from families E-G exhibited some or all of these features. Plasma samples were obtained from sodium citrate anticoagulated blood by centrifugation and saved at –70°C as previously described (Tsai, H.M. & Lian, E.C.Y [1998] N. Engl. J. Med. *339*, 1585-1594). Mononuclear cells were obtained from heparin anticoagulated blood by centrifugation on Ficoll-Hypaque, washed and transformed with Epstein-Barr virus. Informed consent was obtained from all individuals prior to sample collection following an Institutional Review Board approved study protocol.

B. VWF-cleaving protease activity of patient sera. For the measurement of VWF-cleaving protease activity, guanidine hydrochloride-treated VWF was used as the substrate. Protease activity was represented by the optical density of the dimer of the 176kd fragment generated from the VWF substrate (Tsai, H.M. & Lian, E.C.Y. [1998] N. Engl. J. Med. *339*, 1585-1594) and was expressed in U/mL, with the activity measured in pooled normal control plasma defined as 1 U/mL. Each sample was measured on at least three occasions and the mean of the results is presented. Assays for inhibitors of VWF-cleaving protease were performed as described (Tsai *et al.* [2001] Clin. Lab. *47*, 387-392).

C. Haplotype analysis. A total of 17 markers were used for haplotype analysis . 13 of these markers were obtained from the comprehensive genetics maps of Genethon (Dib, C. *et al.* [1996] Nature *380*, 152-154) and Marshfield (Broman, K.W. *et al.* [1998] Am. J. Hum. Genet. *63*, 861-869), and 4 of these markers were designed from sequence repeat information available at http://genome.ucsc.edu (see Table 3).

Table 3:

New STS markers.

Marker	Accession#	BAC	5' primer	3' primer
GL1-3	pending	AL157938	5'-gctttgctctcctgagcttc-3'	5'-gtggtgcagttcactgtcgt-3'
GL2-1	pending	AL160271	5'-gttgcagtgagctgagatcg-3'	5'-tgcaggggttttatctccta -3'
GL3-2	pending	AL160165	5'-tgggtgacagagcaagactg-3'	5'-cttgtatccacgcacagagg -3'
GL4-1	pending	AC002104	5'-agcctgggtgacagagtgag-3'	5'-tacaccaattccccaggtgt-3'

D. Linkage analysis. A genome-wide linkage screen was performed using 382 polymorphic microsatellite markers spaced an average of 10 cM (panels 1-27 of the ABI Prism Linkage Mapping Set-MD10 (Applied Biosystems)). 20 ng of genomic DNA was amplified using AmpliTaq Gold DNA polymerase (Applied Biosystems). PCR products were run on an ABI Prism 3700 DNA Analyzer and analyzed using Genescan v3.5NT and Genotyper v3.6NT. Inspection of the pedigrees indicated an autosomal recessive mode of inheritance for TTP in this set of families. The frequency of the disease gene was assumed to be one per ten thousand chromosomes in the population. Population frequencies of the marker alleles were estimated from the genotyped individuals. Two-point LOD scores were calculated using the program MLINK as implemented in the FASTLINK package, version 3.0 (Schaffer, A.A. *et al.* [1994] Hum. Hered. *44*, 225-237) using an autosomal recessive model. A second series of analyses was performed using a codominant model to reflect the lowered enzyme levels of individuals who were assumed to be carriers of the disease gene. For the latter analysis, individuals were classified as affected (those with clinical diagnoses), carriers (those with protease levels in the range of 0.45 – 0.68 U/mL) and unaffected (those with protease levels in the range of 0.8 – 1.17 U/mL). Penetrance was set at 100% for both models. Multipoint analyses were performed with the program VITESSE (O'Connell, J.R. & Weeks, D.E. [1995] Nat. Genet. *11*, 402-408), using the same two

disease models and the 5 markers at or flanking the maximum two-point LOD score. Order and distances between markers were determined using the ABI Prism Linkage Mapping Set-MD10 map information.

E. Sequence analysis. All exons and intron/exon boundaries of the predicted *ADAMTS13* gene were amplified from patient genomic DNA with the exception of exon 7, which could not be amplified with multiple primer sets. Intron primers were selected using the Primer3 software package (http://www-genome.wi.mit.edu/cgi-bin/primer/primer3_www.cgi) to allow for analysis of exon sequence as well as flanking donor and acceptor splice sites. (See Table 4 for primer sequences). 100 ng of genomic DNA was used in a PCR reaction using either Platinum Taq DNA polymerase (Invitrogen), the Expand Long-Template DNA polymerase mix (Roche) or the Advantage 2 DNA polymerase mix (Clontech). PCR products were either purified directly from the PCR reaction using the Qiaquick PCR purification kit (Qiagen) or gel-purified from low-melting agarose (Invitrogen) using the Wizard PCR preps purification kit (Promega). Total cellular RNA from lymphoblast cell lines was prepared using Trizol (Invitrogen) and RT-PCR performed using the One-Step RT-PCR kit (Invitrogen), according to the manufacturer's instructions. Sequencing reactions were performed by the University of Michigan DNA Sequencing Core. Selected PCR products were subcloned into a pCR-TOPO plasmid (Invitrogen) for further sequence analysis.

Table 4

Primers used for the amplification of *ADAMTS13* exons and intron/exon boundaries

Exon	Forward Primer Sequence	Reverse Primer Sequence	Annealing Temp.
1	5'-CCC TGA ACT GCA ACC ATC TT-3'	5'-CAA ACC CCA AAG CTG ATG TA-3'	56[1]
2	5'-TCG GTC TCC CCA AGT GTT AG-3'	5'-AAC AGG GTT GAC AGC AGC TT-3'	56[1]
3	5'-TCT AGA ACC ATC GCC CTC TG-3'	5'-CCG AGC CAT TCT ACC TGA GT-3'	56[1]
4	5'-GCC TCT CCA GCT CTT CAC AC-3'	5'-GCA TTC TGT GAT CCA TGC TG-3'	56[1]
5-6	5'-ACG GGC TAG TCA TAG GGT TG-3'	5'-TAC AAG GAC CCA CTG CTT GC-3'	56[1]
7	Not yet available	Not yet available	
8	5'-CTT CCA AAC GCT TCC ATC CT-3'	5'-CCC TCC CAG GAC TAG CTA CA-3'	56[2]
9	5'-TCT GGG AGG GAC AGT TAA GG-3'	5'-TAC TGG TCC TGC CTC CTG AC-3'	56[1]
10-11	5'-GGG ATC CCT ATG GGT GAG TT-3'	5'-CCT GGT GTG AAC CAC AGA TG-3'	56[1]
12	5'-GCA CTT TTG TCA CCC CAG TT-3'	5'-CCA GAG CCT GAA CCA CTT TG-3'	56[2]
13-14	5'-CCC AGA TGC AAA GGA TGA AG-3'	5'-ATC CAG GGC TGA GTG AGT GT-3'	56[1]
15	5'-TTT TTC CCG ACC AGC TAA GA-3'	5'-TCA GAA GTG AGG GCA TCT TG-3'	56[1]
16	5'-CCG GGA AGG AGA GTC ACT G-3'	5'-CCC TGT AAG TGA CCG CTG A-3'	60[1]
17-18	5'-GTG ATT GCT TGC TGA ACG AA-3'	5'-CAG TGT CCT CAC CTG CAG AA-3'	56[1]
19	5'-GAA CAC CTG GAG AGG CTA GG-3'	5'-ACT TAC AAC CGC CAG GTG AC-3'	58[3]
20	5'-GAA CCT GCT GGC TGA TGA AT-3'	5'-GGA TGG TGT TCT TGC TCT GG-3'	56[1]
21	5'-CAC ACA CGC CAC TTC CTG-3'	5'-CCA CGT GTT CCC ATA TAG TCT G-3'	56[1]
22	5'-CAC AGC TGG TAA GTG GCA GA-3'	5'-CAC AGC TGG TAA GTG GCA GA-3'	60[1]
23	5'-TCC CAG CTT CCT GTC TCT TC-3'	5'-TCT CCT GAT TCA GCT TTC CAA-3'	60[1]
24	5'-AGT ACA CGT GGG TGG AGA GG-3'	5'-CTT TCA GGG GAC ACG ATG AG-3'	56[1]
25	5'-TTA ACT GCC TCC CAG CTT GT-3'	5'-CTT TGC CAG GGA GAA AGA GG-3'	56[3]
26-27	5'-ACA GGG TCC ACC CCT ACC T-3'	5'-CCC AGT TCC TTC CAT CTC AG-3'	56[1]
28	5'-TAT TGA CCA CAG TGC CAT GC-3'	5'-TGG TGA ATA TGT GGA GGA AGG-3'	56[1]
29	5'-CCT CGG TTT TCT GGG TAG AG-3'	5'-CCA TCC TCG GAG TGG AAT C-3'	56[1]

[1] PCRs done with Platinum Taq DNA polymerase (Invitrogen)
[2] PCRs done with Expand Long Template DNA polymerase mix (Roche)
[3] PCRs done with Advantage 2 DNA polymerase mix (Clontech)

Genomic DNA was obtained from an additional family. Samples from 2 affected individuals as well as from the parents and 6 unaffected siblings were available for analysis. Amplification and sequence analysis of exons 1-6 and 8-29 and the corresponding exon/intron junctions of the ADAMTS13 gene were performed on genomic DNA from one of the probands as described above. As described above, amplification of exon 7 could not be achieved despite the use of additional primer pairs designed from updated draft genomic sequence. Amplification and sequence analysis of exon 26, in which a C --> T substitution

was identified, was performed on genomic DNA from all other members of this family. Allele-specific oligonucleotide hybridization was performed as described above.

F. Allele-specific oligonucleotide hybridization and restriction digestion. Individual exons were amplified from 92 unrelated control individuals. For allele-specific oligonucleotide hybridization, PCR products were spotted onto nitrocellulose membranes using a dot-blot apparatus (Invitrogen). 15-mer oligonucleotides corresponding to wild-type or mutant alleles were end-labeled with γ-32P-ATP using T4 polynucleotide kinase (New England Biolabs). Hybridization was performed in ExpressHyb solution (Clontech) at 37°C. Blots were washed in 5X SSPE, 0.1% SDS at a temperature determined empirically for each oligonucleotide. For restriction digests, 10 µl of PCR product were digested with enzyme (New England Biolabs), according to the manufacturer's instructions and products analyzed on a 3% NuSieve GTG agarose (BioWhittaker Molecular Applications), 1% agarose (Invitrogen) gel.

G. RT-PCR and Northern blot analysis. RT-PCR analysis was performed on cDNA obtained from a Multiple Tissue cDNA panel (Clontech) using primers 5'-CAGTGCAACAACCCCAGAC-3' and 5'-GGCACCTGTCCCATACCTG-3', which amplify cDNA nucleotides 1265-1636. A First-Choice Human Northern Blot (Ambion) was screened with a probe generated by random priming using the Rediprime II kit (Amersham) of a PCR product amplified from a human MOLT4 T cell cDNA library (generated as previously described (Ginsburg, D. *et al.* [1985] Science *228*, 1401-1406) using the above primers. Hybridization was performed in ExpressHyb solution (Clontech) according to manufacturer's specifications. The final wash step was performed in 0.1X SSC, 0.1% SDS at 50°C.

H. Isolation of cDNA. A human fetal liver cDNA library in λgt10 (Clontech) was screened with the Northern probe described above. Two overlapping cDNA clones were obtained, spanning exons 5-14 and 8-20 of the predicted *ADAMTS13* cDNA sequence, respectively. Phage DNA was purified using a Nucleobond lambda midi kit (Clontech), digested with EcoRI (New England Biolabs) and subcloned into pBSII-SK+ (Stratagene). 5' RACE was performed on RLM-RACE-ready human liver cDNA (Ambion) using the following primers : 5'-GTGTCGTCCTCAGGGTTGAT-3' (outer) and 5'-GGCTCTGTCAGAATGACCATC-3' (inner). Marathon RACE-ready human liver cDNA (Clontech) was used for 3' RACE using primers

5'-TGCCAGGTGGGAGGTGTCAGAG-3' (outer) and 5'-GCCTGGCCTTTGAGAACGAGAC-3' (inner) and for nested RT-PCR using primers 5'-CATTGGCGAGAGCTTCATC-3' and 5'-ATGGGGAGGGAGCCTTCT-3' (outer) and 5'-ACCCTGAGCCTGTGTGTGTC-3' and 5'-GCAGAGGTGGCATCCAGA-3' (inner) to amplify a product spanning cDNA nucleotides 1552-2625. RACE and RT-PCR products were cloned into a pCR-TOPO vector (Invitrogen) and individual clones were subjected to sequence analysis. Sequence bridging that obtained by 5' RACE and that of the overlapping cDNA clones (cDNA nucleotides 389-534) was obtained from the *C9ORF8* EST cluster (Unigene cluster Hs.149184). Exon-intron boundaries and sequence accuracy were verified against available draft human sequence at http://www.ncbi.nlm.nih.gov/.

I. Generation of ADAMTS13 mammalian expression construct and mutants. An *ADAMTS13* cDNA encompassing exons 1-29 was assembled and cloned into the EcoRI and EcoRV sites of pCDNA3.1 (Invitrogen). The cloned fragment corresponds to nucleotides 62-4390 in the *ADAMTS13* cDNA (GenBank accession number AF414401), encompassing the entire *ADAMTS13* coding sequence. The following sequence was inserted into the EcoRI site of the vector in order to include an optimized Kozak consensus sequence (Kozak [1991] J. Biol. Chem. *266*, 19867-19870) (uppercase) 5' - tcgatcctcgagtctagaGCCGCCACCATG - 3', with the underlined ATG serving as the start codon. Nucleotides 1-707 (with the A of the ATG designated +1) were derived from IMAGE EST clone 1874472 (GenBank accession number AI281246); nucleotides 708-896, and 897-1748 were derived from two previously described cDNA clones isolated from a human fetal liver cDNA library (Clontech), nucleotides 1749-2918 and 2919-4329 were derived from previously described RT-PCR and 3' RACE products. An error in the 3' RACE clone (insertion of a G at position 3631 of AF414401) was corrected by site-directed mutagenesis using the GeneEditor mutagenesis system (Promega).

Nine ADAMTS13 missense mutations shown in Table 1 were engineered into the full-length construct by site-directed mutagenesis using the GeneEditor mutagenesis system (Promega).

A construct encoding a C-terminal epitope tagged version of the *ADAMTS13* cDNA was engineered by PCR through the replacement of the sequence spanning the *ADAMTS13* termination codon to the Not I site of pcDNA3.1 in the construct above (encoding exons 1-

29) with the following sequence encoding a FLAG epitope (DYKDDDDK) 5'-gactacaaggacgacgacgacaagtaggcggccgc-3'.

DNA for transfection was prepared using the PerfectPrep plasmid XL (Eppendorf) or Maxi (Qiagen) kits.

J. Transfections. Polyoma T-antigen expressing CHO cells (CHO-Tag) (Smith & Lowe [1994] J. Biol. Chem. *269*, 15162-15171) were cultured in alpha-MEM (supplemented with deoxyribonucleotides and ribonucleotides), containing 10% heat-inactivated fetal bovine serum, 0.4 mg/ml G418, penicillin and streptomycin (Life Technologies). Cells were split into 6-well culture dishes (Costar, 3516) at 6 X 105 cells/well 48 hours before transfection. Transfections were performed in triplicate for each construct . Four mg of each DNA (pcDNA3.1, pCDNA3.1-*ADAMTS13* and pcDNA3.1-*ADAMTS13* mutants 1-9) were introduced into the cells using Lipofectamine 2000 (Invitrogen) according to manufacturer's optimized conditions for CHO-K1 cells. As a transfection control, 25 ng of pSEAP2-Control vector (BD Biosciences), encoding secreted alkaline phosphatase, was co-transfected with each DNA. Cells were washed three times with D-PBS (Life Technologies) and serum-free ∀-MEM was added 18 hours following transfection. Conditioned media were collected 48 hours following transfection. One milliliter of conditioned media was concentrated approximately 20-fold using Ultrapure-30 columns (Amicon). Secreted alkaline phosphatase activity in 1 ml of concentrated conditioned media was measured using the Great EscAPe SEAP detection kit (BD Biosciences) and read in a TD-20 luminometer (Turner Designs). Volumes of conditioned media were normalized to the sample with the lowest transfection efficiency and equal volumes (10 ml) were used for the measurement of VWF-cleaving protease activity. Secreted alkaline phosphatase activity in conditioned media from cells transfected with pcDNA3.1 alone was 1.9–43 fold higher than in media from cells transfected with the various constructs. The latter controls were thus not normalized for transfection efficiency (samples were used undiluted) in order to obtain the most conservative estimate of background VWF-cleaving protease activity present in conditioned media. When taking into account the concentration factor for each of the wild-type samples (8.5-10.2 fold), and the VWF-cleaving protease activity in conditioned media of cells transfected with wild-type, the *ADAMTS13* construct ranged from 4.2-4.7 U/ml, with 1 U/ml representing the VWF-cleaving protease activity present in pooled normal plasma.

K. VWF-cleaving protease assay of transfected cells. VWF-cleaving protease assays were performed as previously described (Tsai *et al.* [2001] Clin. Lab *47*, 387-392). Assays were performed blindly and in triplicate for each transfection. The activity in 1 ml of pooled normal human plasma was designated as 1 U. The lack of activity in serum-free and serum-replete media was verified. Results shown in Figure 11 represent the means of three transfections for each mutant, with error bars representing standard deviations. Statistical significance was determined using ANOVA.

L. Generation of anti-peptide antibodies. Anti-peptide antibodies against ADAMTS13 were generated and affinity purified by a commercial supplier (Research Genetics). Antibodies were raised in rabbits against the following peptides: 1) SQTINPEDDTDPGHAD (metalloprotease domain), 2) ESFIMKRGDSFLDGTR (cysteine-rich domain), 3) GRLTWRKMCRKLLD (CUB domain), and 4) CPEMQDPQSWKGKEGT (C-terminus). The cysteine at the N-terminus of the last peptide was artificially added for conjugation purposes.

M. Western blot analysis. Conditioned media from CHO-Tag cells transfected with wild-type and mutant *ADAMTS13* constructs, or mock-transfected with empty pcDNA3.1 vector, were subjected to SDS-PAGE and transferred to nitrocellulose membranes. Membranes were blocked in 5% powdered milk in PBS and incubated with anti-peptide antibodies (1:500) or anti-FLAG M2 monoclonal antibody (Sigma, 1:500). Membranes were then washed in TBS-Tween and incubated with either HRP-conjugated goat anti-rabbit (Sigma, 1:5000) or HRP conjugated goat anti-mouse (Sigma, 1:10,000). Chemiluminescent detection was performed using ECL reagent (Amersham).

N. All publications and patents mentioned in the above specification are herein incorporated by reference. Various modifications and variations of the described method and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in chemistry, and molecular biology or related fields are intended to be within the scope of the following claims.

What is claimed is:

1. A method of identifying subjects at risk of developing TTP disease comprising:

a) providing nucleic acid from a subject, wherein the nucleic acid comprises a *ADAMTS13* gene; and

b) detecting the presence or absence of one or more variations in the *ADAMTS13* gene.

2. The method of Claim 1, further comprising step c) determining if the subject is at risk of developing TTP disease based on the presence or absence of the one or more variations.

3. The method of Claim 1, wherein the variation is a single nucleotide polymorphism.

4. The method of Claim 1, wherein the variation causes a frameshift mutation in *ADAMTS13*.

5. The method of Claim 1, wherein the variation causes a splice mutation in *ADAMTS13*.

6. The method of Claim 1, wherein the variation causes a nonconservative amino acid substitution ADAMTS13.

7. The method of Claim 1, wherein the variation is selected from the group consisting of the mutations shown in Table 1.

8. The method of Claim 1, wherein the detecting in step b) is accomplished by hybridization analysis.

9. The method of Claim 1, wherein the detecting in step b) comprises comparing the sequence of the nucleic acid to the sequence of a wild-type *ADAMTS13* nucleic acid.

10. A method of identifying subjects at risk of developing TTP disease comprising:

a) providing a blood sample from a subject, wherein the blood sample comprises an ADAMTS13 protease; and

b) detecting the presence or absence of one or more variants of the ADAMTS13 protease.

11. The method of Claim 10, wherein the detecting in step b) is accomplished by an antibody assay.

12. A kit for determining if a subject is at risk of developing TTP disease comprising a detection assay, wherein the detection assay is capable of specifically detecting a variant *ADAMTS13* allele.

13. The kit of Claim 12, wherein the detection assay comprises a nucleic acid probe that hybridizes under stringent conditions to a nucleic acid sequence comprising at least one mutation selected from the group consisting of the mutations shown in Table 1.

14. A kit for determining if a subject is at risk of developing TTP disease comprising a detection assay, wherein the detection assay is capable of specifically detecting a variant ADAMTS13 protease.

15. The kit of Claim 14, wherein the detection assay comprises an antibody capable of binding to an ADAMTS13 protease selected from the group consisting of wild-type proteases and proteases comprising at least one amino acid mutation shown in Table 1.

16. An isolated nucleic acid comprising a sequence encoding a polypeptide selected from the group consisting of SEQ ID NOs: 2 and 4 and variants of SEQ ID NO:2 as shown in Tables 1 and 2.

17. The nucleic acid sequence of Claim 16, wherein the sequence is operably linked to a heterologous promoter.

18. The nucleic acid sequence of Claim 17, wherein the sequence is contained within a vector.

19. A host cell comprising the vector of Claim 18.

20. The host cell of Claim 19, wherein the host cell is selected from the group consisting of animal and plant cells.

21. The host cell of Claim 20, wherein the host cell is located in an organism.

22. An isolated nucleic acid sequence comprising a sequence selected from the group consisting of SEQ ID NOs: 1 and 3 and variants of SEQ ID NO:1 as shown in Tables 1 and 2.

23. A computer readable medium encoding a representation of the nucleic acid sequence of claim 22.

24. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 2 and 4 and variants of SEQ ID NO:2 as shown in Tables 1 and 2.

25. A computer readable medium encoding a representation of the polypeptide of claim 24.

26. A method of identifying subjects at risk of carrying an allele for TTP disease comprising:

a) providing nucleic acid from a subject, wherein the nucleic acid comprises a *ADAMTS 13* gene; and

b) detecting the presence or absence of one or more variations in the *ADAMTS13* gene.

27. The method of Claim 26, further comprising step c) determining if the subject is at risk of carrying TTP disease based on the presence or absence of the one or more variations.

28. An isolated nucleic acid comprising a sequence encoding a polypeptide CUB domain of ADAMTS13.

29. The isolated nucleotide of Claim24 comprising SEQ ID NO: 5.

30. An isolated polypeptide comprising a CUB domain of ADAMTS13.

31. The isolated polypeptide of Claim 30 comprising SEQ ID NO: 6.

32. A method of treating a patient with TTP disease, comprising administering a therapeutically effective amount of an ADAMTS13 protease such that the symptoms of the disease are alleviated, wherein the ADAMTS13 protease is selected from the group consisting of: recombinant ADAMTS13; synthetic ADAMTS13; mutants, variants, fragments, and fusions of recombinant ADAMTS13; and mutants, variants, fragments, and fusions of synthetic ADAMTS13.